

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: September 4, 2002, 16:12:45 : Search time 101.54 Seconds  
(without alignments)  
444.770 Million cell updates/sec

Title: US-09-052-089a-2  
Perfect score: 2393  
Sequence: 1 MPILSLCTICSDFFDHSRDV.....VRITVSSASQPKLDFLQ 470

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	919	38.4	433	2 T30807	TRAF interacting p
2	221	9.2	506	2 F85016	probable RING zinc
3	204.5	8.3	425	2 T23457	hypothetical prote
4	200.5	8.4	1690	2 T13030	microtubule bindin
5	192.5	8.0	1325	2 T42722	male-enhanced anti
6	191.5	8.0	2139	2 T18296	myosin heavy chain
7	190	7.9	2017	1 A36014	myosin heavy chain
8	190	7.9	2057	2 E61477	myosin II heavy ch
9	186.5	7.8	1156	2 E69444	chromosome segrega
10	186.5	7.8	1940	1 E04090	myosin heavy chain
11	185.5	7.8	1039	2 S18199	myosin heavy chain
12	185.5	7.8	1940	1 A24922	myosin heavy chain
13	185.5	7.8	2116	2 A26655	myosin heavy chain
14	183	7.6	1938	2 A40997	myosin heavy chain
15	182.5	7.6	501	2 A38650	myosin heavy chain
16	181	7.6	1156	2 B70356	chromosome assembl
17	181	7.6	2007	1 B43402	myosin heavy chain
18	180	7.5	1992	1 S02771	myosin heavy chain
19	179.5	7.5	1961	1 A61231	myosin heavy chain
20	179.5	7.5	1976	2 A59252	myosin heavy chain
21	179	7.5	1017	2 PC4035	cell-cycle-depende
22	178.5	7.5	1999	1 S21801	myosin heavy chain
23	178	7.4	1957	2 S67593	transport protein
24	177.5	7.4	1957	2 T38077	hypothetical colle
25	177	7.4	2168	1 T30171	ninein - mouse
26	176.5	7.4	1509	1 A27224	myosin heavy chain
27	176.5	7.4	1827	2 T16270	hypothetical prote
28	176	7.4	389	2 B44972	paramyosin - nemat
29	175.5	7.3	1133	2 T22976	hypothetical prote

30	175	7.3	866	2 S04027	paramyosin - Caeno
31	175	7.3	872	2 T19296	hypothetical prote
32	175	7.3	1177	2 B75150	chromosome segrega
33	175	7.3	1313	2 F96673	hypothetical prote
34	174.5	7.3	3225	2 T52300	giantin - human
35	174.5	7.3	3259	1 A56539	giantin - human
36	174	7.3	676	2 S00084	myosin heavy chain
37	173.5	7.3	1203	2 B55094	chromosomal protei
38	172.5	7.2	1313	2 A48467	myosin heavy chain
39	172.5	7.2	1937	2 T38055	myosin heavy chain
40	171.5	7.2	853	2 T51505	hypothetical prote
41	171.5	7.2	876	2 A23767	myosin heavy chain
42	171.5	7.2	1957	2 A59294	skeletal myosin -
43	171	7.1	1130	2 T34081	hypothetical prote
44	171	7.1	1738	2 T14867	interapitin - slime
45	171	7.1	1964	2 A59282	nonmuscle myosin I

ALIGNMENTS

RESULT 1

T30807 TRAF interacting protein - Fugu rubripes

C:Species: Fugu rubripes

C:Date: 02-Sep-2000 #sequence\_revision 02-Sep-2000 #text\_change 02-Sep-2000

C:Accession: T30807

R:Cottage, A.J.; Clark, M.; Hawker, K.; Umrana, Y.; Wheller, D.; Bishop, M.; Elgar, F.E.B. Lett. 443, 370-374, 1999

A:Title: Three receptor genes for plasmalogen related growth factors in the genome of

A:Reference number: 220880; MUID:99148833

A:Accession: T30807

A>Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: DNA

A:Residues: 1-433 <COT>

A:Cross-references: EMBL:AJ010317; NID:e1355235; PID:e1355237; PIDN:CAA09084.1

A:Genetics:

A:Gene: TRIP

A:Introns: 33/2; 52/3; 80/3; 94/1; 136/3; 168/2; 206/2; 235/3; 265/3; 310/1; 352/3; 3

Query Match	Score	Match	Length	DB ID	Description
1	919	38.4	433	2 T30807	TRAF interacting p
2	221	9.2	506	2 F85016	probable RING zinc
3	204.5	8.3	425	2 T23457	hypothetical prote
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9	186.5	7.8	1156	2 E69444	chromosome segrega
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18	180	7.5	1992	1 S02771	myosin heavy chain
19	179.5	7.5	1961	1 A61231	myosin heavy chain
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25	177	7.4	2168	1 T30171	ninein - mouse
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28	176	7.4	389	2 B44972	paramyosin - nemat
29	175.5	7.3	1133	2 T22976	hypothetical prote

```
Qy      415 KIGFDGLGGRKFIQPRDITIIRPVVSKSAKSOKVRIKTVSSASQP 463
          :|:||||||| | | | |
Db      372 QSGYDGLGGRKFQIPIHVR-----SEASKPE 401
```

## RESULT 2

probable RING zinc finger protein [imported] - Arabidopsis thaliana  
 C:Species: Arabidopsis thaliana (mouse-ear cress)  
 C:Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 16-Feb-2001  
 C:Accession: F85016  
 R:anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Spring  
 Nature 402, 769-777, 1999  
 A:Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.  
 A:Reference number: A85001; MUID:20083488  
 A:Accession: F85016  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-506 <STO>  
 A:Cross-references: GB:NC\_001268; NID:g7267624; PIDN:CAB80936.1; GSPDB:GN00140  
 C:Genetics:  
 A:Gene: AT4g01270  
 A:Map position: 4

Query Match	9.28	Score	221	DB 2:	Length	506	••
Best Local Similarity	21.98	Pred. NO.	0.00019				
Matches 120; Conservative	79;	Mismatches	193;	Indels	156;	Gaps	24

QY	5	SICITCSO----	PFHSDVAIHCGHFNHJOLQIOWETAPS----	PRCCORCIQOVBKT	57
Db	10	AICSCICYDCLKPVYENQJISIA--	CGHVFHLCIQOIMEYQSPYNNKRCPLCKQKCSIKD		67
QY	58	IINKLFPDLAEEBNVL-----	DAEFLKNEIDSVKAL-----	SQKREKRSOAI	104
Db	68	PCRLYFSSGNGQJTSIASDKVVGIEEDPVLLRGVCKRLECGVQVULJTALEKKKENVEYS			127
QY	105	DTLRDTLE-----	ERNATYESIQNALNKAEMLCSTLKQOMKPLEQRODETQOARE*		154
Db	128	DKLHOCNOLKEDKVRKWEALQEIISTQHLIKLKESEECIQINSOCVKIQER---	TALAK		184
QY	155	EAHRKJC-----	KKMTMEQIEILLQS----	QBSRVEEMIR--	DMGV 185
Db	185	ELASIKLKVSDLSLEEDVYKTLALLGNNAKTKOTIDTLVKSXVIRNNKSKTELLACNODGR			244
QY	190	GQS-AVEOLAVYCVSLKKEYENLKEARKATGELADRLKLDVSSRSRLKLTINTELDOAKL			248
Db	245	GEANSSERLEKALEKIEKLRKRMLELITEERENRALROJNVSK---	KCYTEVSEPAI		301
QY	249	ELRSQKDLQASADOEITSLRKSDDPQGNLEPASATNVTYSRLVESPAPYEMMNPRLHQ			306
Db	302	ESMSFRML-TSSDNKV-----	EKISTPGKLEEKDGFIIQSGCL-----	RGRE	343
QY	309	PPFGDEIDLNTFPYVN--	PPPTQSG-----	SQGCPLKIKLCLEBARSPMGNVL	354
Db	344	DSEYFSRD--	SVIDVDDYVPETNITSGIRDMWNTEIEKGDSQWYKDKIFNIRKQPTSSV-		400
QY	355	KKVHVSKPESQ-----	LSLGGORCVG-----	ELDELAGAPPLFIIRNAVILQOK	399
Db	401	-----	SPYSNGSGNIMOSSGTRNRIJGSRWMSKHGERNEATPSSLOGSVP-		441
QY	400	PNRFTAESRSTDVYRIGFDGLGRTRYFIQPRDTTIIIRPVYVSKASAKSQ-----	KVRI		453
Db	442	-----	RKDDILISIGDPDGKGRIK-----	VLRSPQISKTUWASSGSGKRFILGT	484
QY	454	KTVSSASQ	461		
Db	485	TTSGSSSQ	492		

RESULT 3  
T25457  
hypothetical protein B0432.9 - *Caenorhabditis elegans*

C:Species: *Cenorhabditis elegans*  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 02-Sep-2000  
C:Accession: J25457  
R:Henkhaus, J.; Wohlmann, P.  
submitted to the EMBL Data Library, December 1996  
A:Description: The sequence of *C. elegans* cosmid B0432.  
A:Reference number: 220038  
A:Accession: J25457  
A:Status: preliminary; translated from GB/EMBL/DDJ  
A:Molecule type: DNA  
A:Residues: 1-425 <HEN>  
A:Cross-references: EMBL:U080836; PIDN:AAB37893.1; GSPDB:GN00020; CESP:B0432.9  
A:Experimental source: strain Bristol N2; clone B0432  
C:Genetics:  
A:Gene: CESP:B0432.9  
A:Map position: 2  
A:Introns: 64/3; 99/3; 165/1; 267/3; 350/2; 386/2  
C:Superfamily: RING finger homology  
E:188-238/Domain: RING finger homology <RRN>

Query Match	8.5%	Score 204.5;	DB 2;	Length 425;
Best Local Similarity	25.9%;	Pred. No. 0.0011;		
Matches 73;	Conservative 49;	Mismatches 105;	Indels 55;	Gaps 12;

[illegible]

RESULT 4  
T13030  
microtubule binding protein D-CLIP-190 - fruit fly (*Drosophila melanogaster*)  
C:Species: *Drosophila melanogaster*  
C:Date: 13-Aug-1999 #sequence\_revision 13-Aug-1999 #text-change 17-Nov-2000  
C:Accession: T13030  
R:Iantzu, V.A.; Miller, K.G.  
J. Cell Biol. 140, 897-910, 1998  
A:Title: A class VI unconventional myosin is associated with a homologue of a microtu  
A:Reference number: 217588; MUID: 98135549  
A:Accession: T13030  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-1690 <LAN>  
A:Cross-references: EMBL:AF041382; NID:g2773362; PID:g2773363; PIDN:AAB96783.1  
A:Experimental source: strain Oregon R  
C:Genetics:  
A:Cross-references: FlyBase:FBgn0020503  
C:Keywords: cytoskeleton

	Query Match	8.4%;	Score	200.5;	DB	2;	Length	1690;
	Best Local Similarity	22.7%;	Pred.	No.	0.0085;			
	Matches	109;	Conservative	73;	Mismatches	168;	Indels	131;
	Gaps	18;						
OY	50 RIQVKKTIINKLPFDLADQEEENVDAEFLKNE-----LDSSVKQLDSOKRREKDDSOAI	103						
	::::: :::	:	: :	: : :	: :	:	:	:

Dh 724 QIOLEKESIEOIAL-----KONELE-DFOKKOSESEVNILOETIKANTOKOLELIVESGES 777  
Qy 104 IDTLRDLFEERNATVESLONALINKAEMICSTIKROM-KFLEORODETKOAREAHRLCK 162  
Dh 778 LKRIQOOLEEETTLGHEKLOALEE-----LKKEKETIIEKEQOELQOOSKAESESA 830  
Qy 163 MKTME-QIELLLOSQSEVEEMIRDMGVGOSAVBOLAVVCSLKEKEYENLEKARKATGEL 221  
Dh 831 LKVVOVLEQLOQOQAAASGEE-----GSKTVAKLHDEISQLKSQAEBETOSKLTJESN 883  
Qy 222 ADRLKRLVSSRSKLK-----TLNTELDQAKLELSAQKODLOSADQETSLKKSDDP 274  
Dh 884 LEAKSQOLEANGSLSEBEAKSGOLOEQITIKLSEVEBETOALASVHTDVESTKQO---- 939  
Qy 275 PGNLEPASATNETVSRLVESP-----PVEKMNPRLO-----PPF 311  
Dh 940 -----LEAANMALEKYNKAEASRAESALQDKVKETITDLHAELOAKRSSSALHTKLKSF 996  
Qy 312 GDEI-----DLNTTFDVNTPPTQTSQSOHCLPKKLCLERARSPMO----- 351  
Dh 997 SDEIATGHKELTSKAD-----AMSQEMLOKKEKLELOELRQOLQDSQDSQTKLKAGER 1048  
Qy 352 -----NVLKVKVSKPESQSLSGORCVGELDELAGAPFLFIRNAVVGOKOPN 401  
Dh 1049 KEKSFESIKMLQOEVTAKTENLELSTGTQTTIKLQOERLE-----ITNAELQHK--- 1099  
Qy 402 RTTASRSSTDVVRIGFDGLGRTKFIQPRD-TTIIRPVVPSKAKSKQVKRITVSAS 460  
Dh 1100 -----EKMASEDAOKIA-----DLKTLVEAIOVANINISATNAELSTVLEVL 1141  
Qy 461 Q 461  
Dh 1142 Q 1142

RESULT 5  
T42722  
male-enhanced antigen-2 - mouse  
C:Species: Mus musculus (house mouse)  
C>Date: 11-Jan-2000 #sequence\_revision 11-Jan-2000 #text\_change 11-Jan-2000  
C:Accession: T42722  
C:Accession: M.; Sutou, S.  
R:Kondo, M.; Sutoh, S.  
DNA Seq: 7, 71-82, 1997  
A:Title: Cloning and molecular characterization of cDNA encoding a mouse male-enhanced  
A:Reference number: Z224242; MUID:97217683  
A:Accession: T42722  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-1325 <CON>  
A:Cross-references: EMBL:D78270; NID:d1096175; PID:d1020389; PIDN:BAAI19612.1  
A:Experimental source: strain CD-1  
C:Function:  
A:Description: supposed to play some role for spermatogenesis  
C:Keywords: leucine zipper

Query Match 8.0%; Score 192.5; DB 2; Length 1325;  
Best Local Similarity 22.4%; Pred. No. 0.017;  
Matches 94; Conservative 80; Mismatches 136; Indels 89; Gaps 16;

Qy 65 DLAOEEENVLDA-EFLKNE-----LDSVKAOLSQDKREKR-----DSQAIIIDTLRD 109  
Dh 590 ELOREADSRDAIHRLQNEKLVLEVALQSAKDELDRGARLEEDTEETSGLEQLRQ 649  
Qy 110 TLBERNATVESLONALINKAEMICSTIKROM-KFLEQ-----RODET-----KQ 151  
Dh 650 DLAVKSNQVEHLQOE-----TATLRQOKQVKEQFOQOQVWVEAYVRATSKDOLINE 702  
Qy 152 AREEHNRLCKCMKMTMEQIELLLOSORSVE-----EMIRDMGVGOSAVBOLAVVCSLKE 207  
Dh 703 LKATKRLDSEMKELRQELIKLOGEKKTVEVHSHQLQDKMSLVHQQAMELGSHLOSVOKE 762  
Qy 208 YEN-----LKEA-----RKATGELADRLKDLVSSRSKLTNTLNTLDOA 246

Dh 763 RDEMEIHLQSLKFKDEQIMALTAEANETLAKQIPELOEOAKKATTEQOKKKRIGSDLTSA 822  
Qy 247 KLELSAQKODLOSADQETSLRKSDPRPNLEPASATNTVRLVESPAPVEMNPR 306  
Dh 823 OKREKTKHKAIVENA-----VSTLSRRLQEA-----LASKRETKDELQOLRQOSTG--GSSDPVL 874  
Qy 307 HOPPFGEIDILNTT-----PDVNPPTQTSQSOHCLPKKLCLERARSPMOVLKV 357  
Dh 875 HEKIRALEVELQNVGOSKILLEKELOEVTIMTQOELSESEKYLELEDELOESRGFRKI 934  
Qy 358 HVSQSPESQSLSGORCVGELDELAGAPFLFIRNAVVGOKOPNRTTAESSRSSTDVRI 416  
Dh 935 KRLSESNKLTAL-----ELEHERGKLTGQSNALREHNSILETALAKREADIVOL 986

RESULT 6  
T18296  
myosin heavy chain - Entamoeba histolytica  
C:Species: Entamoeba histolytica  
C>Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 08-Sep-2000  
C:Accession: T18296  
R:Guillen, N.  
Submitted to the EMBL Data Library, February 1997  
A:Reference number: Z18865  
A:Accession: T18296  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-2139 <GUI>  
A:Cross-references: EMBL:L03534; NID:g1850912; PID:g1850913; PIDN:AA848065.1  
C:Genetics:  
A:Gene: mhca  
A:Superfamily: myosin heavy chain; myosin motor domain homology  
F:91-780/Domain: myosin motor domain homology <CMO>

Query Match 8.0%; Score 191.5; DB 2; Length 2139;  
Best Local Similarity 22.1%; Pred. No. 0.032;  
Matches 97; Conservative 83; Mismatches 161; Indels 97; Gaps 16;

Qy 66 LAOEEENVLDAEFLKNELDVYKAOLSK-----DREKRDQAIIIDTLRDLFEERNATV 118  
Dh 1671 VAOEERK-----QRLSDIAELKELOEERTTAANAEEARKKIQAEIDVEVFNLEDVTNR 1726  
Qy 119 EST--ONALINKAEMICSTIKKOMKLEORODETKOAREEAHRLCKMKMTMEQIELLQSO 176  
Dh 1727 EKLVAKNSENDAEI--DSLKEEKALE--DELEKITDNNKLS-----EIDSIDRKY 1775  
Qy 177 RSEVEEMIRDMGVGOSAVEQLAVVCSLKEKEYENLEKARKATGELADRLKDLVSSRSKL 236  
Dh 1776 NALLDSKSDSVSMKEKFODELKVTYKDALFETKKHNAETMLRG-----RLEKAAEAVGVRL 1831  
Qy 237 KTLNTELDQAKLELSAQKODLOSADQETSLRKSDPRPNLEPASATNTVSRVLESP 296  
Dh 1832 EALQKNLDLAQOEKAKATKQVRAADGELKSLMELDVKQDLDA----- 1876  
Qy 297 APVEMMNPRLHOPPFGEIDILNTTF-----VNTPPTQTSQSOHCLPKKLCLF-----R 345  
Dh 1877 -----QDLDLDEDLATLQDKYKTLVQKQSVFDSRIQ--MOBOLDEKKAGRAK 1924  
Qy 346 ARSPQNVLLKVVHVSQSPESQSL-----SLGQORCVGELDELAGAPFLFIRNA 393  
Dh 1925 AQOKQAVERKKLQLOENDNDFEYKFTADKRITLSAQK--DDLQLOEL-----EK 1973  
Qy 394 VLQOKOPNRTTAE-----SRSTDVVRIGFDGLGRTKFIQPRDITIRPVVPSKAKS 447  
Dh 1974 ERGLKQDSEKEVQRLRVKCOELFETKVAEVG--GANVSIKAKVKAIEADIELTTEADAL 2031  
Qy 448 KQVKRITVSSASOPKID 465  
Dh 2032 KAKKMAEKKAKTSQKID 2049

```
RESULT 7
A36014
myosin heavy chain, nonmuscle - fruit fly (Drosophila melanogaster)
N:Contains: myosin ATPase (P3.6.1.32)
C:Species: Drosophila melanogaster
C:Date: 31-Dec-1993 #sequence, revision 31-Dec-1993 #text, change 19-Jan-2001
C:Accession: A36014; B36014
R:Ketchum, A.S.; Stewart, C.T.; Stewart, M.; Kiehart, D.P.
Proc. Natl. Acad. Sci. U.S.A. 87, 6316-6320, 1990
A:Title: Complete sequence of the Drosophila nonmuscle myosin heavy-chain transcript: cDNA
A:Reference number: A36014; MUID:90349606
A:Accession: A36014
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-2017 <KET>
A:Cross-references: GB:M35012
C:Genetics:
A:Gene: FlyBase:zip
A:Cross-references: FlyBase:FBgn0005634
C:Superfamily: myosin heavy chain; myosin motor domain homology
C:Keywords: actin binding; alternative splicing; ATP; coiled coil; hydrolase; methylated
F:1-2017/Product: myosin heavy chain, form I #status predicted <MA1>
F:4-2017/Product: myosin heavy chain, form II #status predicted <MA2>
F:135-815/Domain: myosin motor domain homology <MMOT>
F:225-232/Region: nucleotide-binding motif A (P-loop)
F:598-631/Region: actin binding #status predicted
F:705-727/Region: actin binding #status predicted
F:888-2017/Domain: coiled coil #status predicted <COI>
F:888-1328/Region: S2
F:1129-2017/Region: light meromyosin
F:116/Modified site: N6, N6, N6-trimethyllysine (Lys) #status predicted
F:231/Binding site: ATP (Lys) #status predicted
F:745,755/Active site: Cys #status predicted
```

```
Query Match 7.9%; Score 190; DB 1; Length 2017;
Best Local Similarity 23.8%; Pred. No. 0.036;
Matches 88; Conservative 61; Mismatches 145; Indels 76; Gaps 14;

QY 56 KTIINKLFFDLQAEENVLDAE--FLKNELDSVKAQLSOKRERKDSQ-----AI 103
DB 1263 KTVLEK-----AKGTLEENADLATELRSVSSNGENDRRKQAESQIAELQVKLAE 1314
QY 104 IDTLRDTLEER---NATVESLONALNKAEMLCSTLKKOMFLERODETKQAREEAHR- 158
DB 1315 IERARSELQEKCTKIQOEAENITNQLEAEELKASAAVKSASNMESQULEAQQLLEETRRQ 1374
QY 159 ---LKCKMKTMEQIELLQSORSEVEEMIRDMGVGQSAVEQLAVYCVSLKREYNLEEAR 215
DB 1375 KLGLSSKLRQIESERKALQOELEEDDEAKRNY---EKRLAEVTTQOMQEIKKAEEDADLA 1431
QY 216 KATGELADRLKDKLVSSRSKLT--NTELDAKLELRSAQKD---LOSADQETSLR 268
DB 1432 KELEGGKRLKDKIDLEARQVKELIAQNDRDKSKKIQSLELATTELEAQRKTVLELE 1491
QY 269 KKSDDPPGNLEPASATMETVSRVLFESPAPVEMNPRLOHPFDEIDLNTFPVNTPTPT 328
DB 1492 KKQK---NPKILAEKKAISEQIAQERDTAREAREKETKVLVSRLDEAFD----- 1541
QY 329 QTSQSQHCLPKKICLERARSPMNVL-----KVVHKVSKP---ESQLS-LGGQ 372
DB 1542 -----KIEDLENKRRKTLQNELDLANTQCTADKNVHELKAKRALESQIAELKQ 1591
QY 373 RCVGELDEEL 382
DB 1592 N-BELEDL 1599
```

```
RESULT 8
S61477
myosin II heavy chain, non-muscle - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C:Date: 19-Jul-1996 #sequence, revision 26-Jul-1996 #text, change 02-Feb-2001
```

```
C:Accession: S61477; S65349
R:Mansfield, S.G.; Al-Shirawi, D.Y.; Ketchum, A.S.; Newbern, E.C.; Kiehart, D.P.
J. Mol. Biol. 255, 98-109, 1996
A:Title: Molecular organization and alternative splicing in zipper, the gene that enc
A:Reference number: S61477; MUID:96144835
A:Accession: S61477
A:Molecule type: DNA
A:Residues: 1-2057 <MAN>
R:Cross-references: EMBL:U35816
R:Mansfield, S.G.; Al-Shirawi, D.Y.; Ketchum, A.S.; Newbern, E.C.; Kiehart, D.P.
submitted to the EMBL Data Library, September 1995
A:Reference number: S65349
A:Accession: S65349
A:Molecule type: DNA
A:Residues: 1-1908 'NL', 1911-2057 <MAN>
A:Cross-references: EMBL:U35816; NID:91141789; PIDN:AMB09049.1; PID:91572481
C:Genetics:
A:Gene: zip
A:Cross-references: FlyBase:FBgn0005634
A:Introns: 10/3; 90/3; 162/3; 215/1; 255/3; 263/3; 303/3; 334/3; 1248/1; 1349/3; 1526
C:Superfamily: myosin heavy chain; myosin motor domain homology
C:Keywords: alternative splicing; ATP; nucleotide binding; P-loop
F:135-855/Domain: myosin motor domain homology <MMOT>
F:225-232/Region: nucleotide-binding motif A (P-loop)
```

```
Query Match 7.9%; Score 190; DB 2; Length 2057;
Best Local Similarity 23.8%; Pred. No. 0.037;
Matches 88; Conservative 61; Mismatches 145; Indels 76; Gaps 14;

QY 56 KTIINKLFFDLQAEENVLDAE--FLKNELDSVKAQLSOKRERKDSQ-----AI 103
DB 1303 KTVLEK-----AKGTLEENADLATELRSVSSNGENDRRKQAESQIAELQVKLAE 1354
QY 104 IDTLRDTLEER---NATVESLONALNKAEMLCSTLKKOMFLERODETKQAREEAHR- 158
DB 1355 IERARSELQEKCTKIQOEAENITNQLEAEELKASAAVKSASNMESQULEAQQLLEETRRQ 1414
QY 159 ---LKCKMKTMEQIELLQSORSEVEEMIRDMGVGQSAVEQLAVYCVSLKREYNLEEAR 215
DB 1415 KLGLSSKLRQIESERKALQOELEEDDEAKRNY---EKRLAEVTTQOMQEIKKAEEDADLA 1471
QY 216 KATGELADRLKDKLVSSRSKLT--NTELDAKLELRSAQKD---LOSADQETSLR 268
DB 1472 KELEGGKRLKDKIDLEARQVKELIAQNDRDKSKKIQSLELATTELEAQRKTVLELE 1531
QY 269 KKSDDPPGNLEPASATMETVSRVLFESPAPVEMNPRLOHPFDEIDLNTFPVNTPTPT 328
DB 1532 KKQK---NPKILAEKKAISEQIAQERDTAREAREKETKVLVSRLDEAFD----- 1581
QY 329 QTSQSQHCLPKKICLERARSPMNVL-----KVVHKVSKP---ESQLS-LGGQ 372
DB 1582 -----KIEDLENKRRKTLQNELDLANTQCTADKNVHELKAKRALESQIAELKQ 1631
QY 373 RCVGELDEEL 382
DB 1632 N-BELEDL 1639
```

```
RESULT 9
E69444
chromosome segregation protein (smc1) homolog - Archaeoglobus fulgidus
C:Species: Archaeoglobus fulgidus
C:Date: 05-Dec-1997 #sequence, revision 05-Dec-1997 #text, change 02-Jun-2000
C:Accession: E69444
R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dod
.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A:Authors: Uterback, T.; Cotton, M.D.; Spriggs, T.; Artlich, P.; Kaibe, B.P.; Sykes,
Smith, H.O.; Woese, C.R.; Venter, J.C.
A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing arch
A:Reference number: A69250; MUID:98049343
```

A:Accession: E69444  
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-1156 <LIE>  
 A:Cross-references: GB:AE000995; GB:AE000782; NID:g2689318; PIDN:AA88690.1; PID:g264900  
 C:Superfamily: chromosome segregation protein SMCI

Query Match 7.8%; Score 186.5; DB 2; Length 1156;  
 Best Local Similarity 16.7%; Pred. No. 0.029;  
 Matches 78; Conservative 111; Mismatches 152; Indels 125; Gaps 13;

QY 55 KTIINKLFFDLAGEENVL---DAEFLKNE----- 82  
 Db 671 KERMLSVKIIYQREKRGFLAEFLNRASLRQYKDEVDRLTGMISELRNRLSLDEKIRT 730  
 QY 83 -----LDSVKQQLSKQDKK-----RDSQAIITLDTLEERRATVESLONALNKAEML 131  
 Db 731 ESGRIEELREKISQSKREKENVYISLKDYNKSIAEMEAIGELAEIEIERMLRGE-- 788  
 QY 132 CSTLKQKMFLEQRQDETQKQAREAHRLKCKMKT---EQIELLLQSO-----RSEV 180  
 Db 789 ---VPKIVEELDKKEHQNRRELISIEKKIESLEFKRQLESSEMQEKVYIDEIKDRI 845  
 QY 181 EEMIRDMGVQSAAVEQLAVYCVSLKKEYENLKARKATGELADRLKKDLVSSRSKLTN 240  
 Db 846 DEIRRTIEEGKARVEEINSELELRKEBELGKLRKRDLEIKQLNRVAEEKKRIE 905  
 QY 241 TELDQALELRSAOKDQASQDETSLRKSSDPPGULEPASATNEVSRIVFESSPAVE 300  
 Db 906 AEIDRLERIKLOERLEISELAEIGEV--EVPENMLPLEKVEKYLDEVL----- 955  
 QY 301 MMNRLQHPGPDIDINTFNTVPTQ-----TSGSQHCLPKCLERARSPMOWLK 355  
 Db 956 -----VELSTEDVNLKAIQEEYKARKADELVEKKMLEKRA---DILD 998  
 QY 356 KVHKVSPESQSLSGRCVGEDELAEAGPLFIRNAVIGOKOPNRTTASRSSTDVVR 415  
 Db 999 RIEKYEKKREI-----PFEVF-----TAINRFALFIR 1027  
 QY 416 IGFGGLGRTKFTIOPRTTIRPPVVKSKAKSKOKVRIKYSSASQ 461  
 Db 1028 ---ELANGEGELYLDSDPFNSGLYIKVKNPKPKVOKLESMSGCK 1070

RESULT 10  
 S04090  
 myosin heavy chain 3, skeletal muscle, embryonic - human  
 N:Contains: myosin ATPase (EC 3.6.1.32)  
 C:Species: Homo sapiens (man)  
 C:Date: 31-Dec-1993 #sequence, revision 31-Dec-1993 #text, change 19-Jan-2001  
 C:Accession: S04090, S06146, S05442, S12460, S09333, A35082  
 R:Eller, M.; Stedman, H.H.; Sylvester, J.E.; Fertels, S.H.; Rubinstein, N.A.; Kelly, A.M.  
 Nucleic Acids Res. 17, 3591-3592, 1989  
 A:Title: Nucleotide sequence of full length human embryonic myosin heavy chain cDNA.  
 A:Reference number: S04090; MUID:89263803  
 A:Accession: S04090  
 A:Status: translation not shown  
 A:Molecule type: mRNA  
 A:Residues: 1-1940 <ELL>  
 A:Cross-references: EMBL:X13988; NID:g34843; PIDN:CAA32167.1; PID:g34844  
 R:Eller, M.; Stedman, H.H.; Sylvester, J.E.; Fertels, S.H.; Wu, O.L.; Raychowdhury, M.K.  
 FEBS Lett. 256, 21-28, 1989  
 A:Title: Human embryonic myosin heavy chain cDNA. Interspecies sequence conservation of  
 A:Reference number: S06146; MUID:90033298  
 A:Accession: S06146  
 A:Molecule type: mRNA  
 A:Residues: 774-1662, 'QT', 1665-1940 <EL2>  
 A:Cross-references: EMBL:X13100; NID:g31143; PIDN:CAA31492.1; PID:g31144  
 R:Karsch-Mizrachi, I.; Trayts, M.; Biau, H.; Leinwand, L.A.  
 Nucleic Acids Res. 17, 6167-6179, 1989  
 A:Title: Expression and DNA sequence analysis of a human embryonic skeletal muscle myosin  
 A:Reference number: S05442; MUID:89366648

A:Accession: S05442  
 A:Molecule type: DNA  
 A:Residues: 856-1390, 'KK', 1393-1940 <KAR>  
 A:Cross-references: EMBL:X15626; NID:g35504; PIDN:CAA3731.1; PID:g1335313  
 R:Stedman, H.H.; Eller, M.; Jullian, E.H.; Fertels, S.H.; Sarkar, S.; Sylvester, J.E.  
 J. Biol. Chem. 265, 3568-3576, 1990  
 A:Title: The human embryonic myosin heavy chain. Complete primary structure reveals e  
 A:Reference number: A35082; MUID:90154023  
 A:Contents: annotation; chromosomal assignment  
 R:Bober, E.  
 submitted to the EMBL Data Library, January 1989  
 A:Reference number: S12458  
 A:Accession: S12458  
 A:Molecule type: mRNA  
 A:Residues: 856-1330, 'G', 1332-1390, 'KK', 1393-1607, 'RA', 1610-1940 <BOB>  
 A:Cross-references: EMBL:X51593; NID:g29463; PIDN:CAA35942.1; PID:g29464  
 A:Experimental source: clone gCMC-E  
 R:Bober, E.; Buchberger-Seidl, A.; Braun, T.; Singh, S.; Goedde, H.W.; Arnold, H.H.  
 Eur. J. Biochem. 189, 55-65, 1990  
 A:Title: Identification of three developmentally controlled isoforms of human myosin  
 A:Reference number: S09331; MUID:90235862  
 A:Accession: S09331  
 A:Molecule type: mRNA  
 A:Residues: 856-901, 'X', 903-971, 'X', 973-1041, 'X', 1043-1111, 'X', 1113-1181, 'X', 1183-125  
 1, 'X', 1673-1741, 'X', 1743-1811, 'X', 1813-1881, 'X', 1883-1940 <BOV>  
 A:Cross-references: EMBL:X51593  
 C:Genetics:  
 A:Gene: GDB:MYH3  
 A:Cross-references: GDB:119443; OMIM:160720  
 A:Map position: 17p13.1-17p13.1  
 C:Superfamily: myosin heavy chain; myosin motor domain homology  
 C:Keywords: actin binding; ATP; coiled coil; hydrolase; methylated amino acid; muscle  
 F:89-767/Domain: myosin motor domain homology <MOTOR>  
 F:119-186/Region: nucleotide-binding motif A (P-loop)  
 F:549-586/Region: actin binding #status predicted  
 F:656-678/Region: actin binding #status predicted  
 F:840-1940/Domain: coiled coil #status predicted <COI>  
 F:840-1280/Region: S2  
 F:1281-1940/Region: light meromyosin  
 F:130/Modified site: N6,N6,N6-trimethyllysine (Lys) #status predicted  
 F:185/Binding site: ATP (Lys) #status predicted  
 F:696,706/Active site: Cys #status predicted

Query Match 7.8%; Score 186.5; DB 1; Length 1940;  
 Best Local Similarity 20.3%; Pred. No. 0.052;  
 Matches 77; Conservative 83; Mismatches 177; Indels 43; Gaps 7;

QY 54 GKTIINKLFFDLAGEENVLDAEFLKNEIDSVKQQLSKQREKRSQAIIIDTLDITL 112  
 Db 1262 GKNEIQRSLSELTQKSRLOTEGELSRQLEKESTVSQLSRKQAFQOTELKQRL 1321  
 QY 113 ERNATVESLONALKAEMLCSTLKKQKFLERQDETQKQAREAH-----RLCKMKMT 166  
 Db 1322 EENKAKNALAHALQSSRHDCDLREQYEEQEGKAEIQRALSKANSEVAQWRTYETDAI 1381  
 QY 167 EQIELLLQSQSEVEEMIRDMGVQSAAVEQLAVYCVSLK-----EYENLKARKATG 219  
 Db 1382 QTELELEPAQ---EKLAQRLODSEQVEAVNAKCALEKTKQRLQSEVEDLWAVVERAN 1437  
 QY 220 ELADRLKKDLVSSRSKKTTLNTELDQAKLELRSAQQLQASQADQETSLRKSSDPPG 279  
 Db 1438 SLAAADLKQKQNFKVLAEKMTKCEQDALEAKESRSLSFLFKLNAYEEALDQLE 1497  
 QY 280 PASATNETVSRFLVESPAVEMNPRILHOPPFGEIDLTNTFDVNTPTQTSQSQCPLP 339  
 Db 1498 TVKRENNLEQEIADLTLEQIENKGTIHE-----LEKSRQIDLEK 1538  
 QY 340 ---RLCLERARSPQONVLKVKHKVSKPESQSLSGRCVGEDELAEAGPLFIRNAVIG 396  
 Db 1539 ADIDLAEAEAALEHBAKRLTQLELTQVKSIEDRKIAEKDEIQLKRNQRTV--- 1595  
 QY 397 QKQPNRTTASRSSTDVVR 416

Db 1596 ETMOSALDAEVRSRNEAIRL 1615

RESULT 11

S18199 myosin heavy chain - chicken (fragment)

C:Species: Gallus gallus (chicken)

C:Date: 22-Nov-1993 #sequence\_revision 26-May-1995 #text\_change 02-Feb-2001

C:Accession: S18199

R:Stewart, A.F.R.; Camoretto-Mercado, B.; Perlman, D.; Gupta, M.; Jakovcic, S.; Zak, R.

J. Mol. Evol. 33, 357-366, 1991

A:Title: Structural and phylogenetic analysis of the chicken ventricular myosin heavy ch

A:Reference number: S18199; MUID:92130260

A:Accession: S18199

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-1039 <STE>

A:Cross-references: EMBL:X59552; NID:962995; PIDN:CAA42130.1; PID:962996

A:Note: in the authors' translation 45-Lys is shown after residue 40, and, consequently,

C:Superfamily: myosin heavy chain; myosin motor domain homology

C:Keywords: ATP; nucleotide binding; P-loop

F:402-409/Region: nucleotide-binding motif A (P-loop)

Query Match 7.8%; Score 185.5; DB 2; Length 1039;  
Best Local Similarity 20.2%; Pred. No. 0.029;  
Matches 77; Conservative 82; Mismatches 167; Indels 55; Gaps 10;

OY 59 INKLFPLDLOEENVL--DAEFLKNEIDSVKAQLSQDKRKRDSQAIIIDTLRLPLEERNA 116

Db 369 MTRLMNDLTQTKTKLQSENGEFVR-OLEEKESLISQLSRGKTSFTQQLIEELRROLEETK 427

OY 117 TVESLONALNKAEMLCSTLKQKMFLEORODETQAREARLRCKMKMTMEQIELLQSO 176

Db 428 SKNALNHLQAARHDCDLRLQYEEEDPAKALQALSKNAEVAQWTKYETDILQTE 487

OY 177 RSE--VEEMIDMGVGSAAVEQLAVYCVSLKKEYENLK-----EARKATGELADRLK 226

Db 488 ELEDAKKKLLARLQEAELAIKANAKCSLEKAKHRLQNEDEMDIMLEKANSAAASLDK 547

OY 227 KDLYSSRSKLTLN--TELDQAKLELSAOKDQADQETLSLRKSSDDPPGULEPASA 283

Db 548 K---QRFQDIINDMKQKYEESQAELEASQKEARSLSTELFKLNAYEETLDLETLKR 603

OY 284 TNETVSRLLVFESPAVEMNRLHOPRGDEIDLTFTFDVTPPTQTSQSGHCLPKICL 343

Db 604 ENKMLQEBISDLTMOISGKNLH-----EIE-----KVKQVEQEKSEVOLAL 647

OY 344 ERARSPMONVLKRYKVKSPESQSLSGQRCVGEIDELAGAFPLFIRNAVIGOKOPART 403

Db 648 EEAGALEHESEKTLRLQLELSQLKADFERKLAKEDEMOMI-----RRNQORT 696

OY 404 -----TAESSRSTDVARI 416

Db 697 IDLSQSTLSEARSNEAIRL 717

RESULT 12

A24922 myosin heavy chain, skeletal muscle, embryonic - rat

N:Contains: myosin ATPase (EC 3.6.1.32)

C:Species: Rattus norvegicus (Norway rat)

C:Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 19-Jan-2001

C:Accession: A24922; A23538; B24263

R:Strehler, E.E.; Strehler-Page, M.A.; Perriard, J.C.; Periasamy, M.; Nadal-Ginard, B.

J. Mol. Biol. 190, 291-317, 1986

A:Title: Complete nucleotide and encoded amino acid sequence of a mammalian myosin heavy

A:Reference number: A24922; MUID:87060988

A:Accession: A24922

A:Molecule type: DNA

A:Residues: 1-1940 <STR>

A:Cross-references: GB:X04267; GB:X05004; NID:956658; PIDN:CAA27817.1; PID:g1619328

R:Strehler, E.E.; Mahdavi, V.; Periasamy, M.; Nadal-Ginard, B.

J. Biol. Chem. 260, 468-471, 1985

A:Title: Intron positions are conserved in the 5' end region of myosin heavy-chain ge

A:Reference number: A22538; MUID:85080119

A:Accession: A22538

A:Molecule type: DNA

A:Residues: 1-168 <ST>

A:Cross-references: GB:L00370; GB:M10135; NID:9205580; PIDN:AAA1655.1; PID:954476

R:Periasamy, M.; Wydro, R.M.; Strehler-Page, M.A.; Strehler, E.E.; Nadal-Ginard, B.

J. Biol. Chem. 260, 15856-15862, 1985

A:Title: Characterization of cDNA and genomic sequences corresponding to an embryonic

A:Reference number: A24263; MUID:86059474

A:Accession: B24263

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1358-1490, 'G' <PER>

A:Cross-references: GB:K03468; NID:9205573; PIDN:AAA1652.1; PID:9205574

A:Experimental source: Clone PMHC-72

C:Genetics:

A:Introns: 68/3; 116/3; 169/1

A:Note: the list of intron positions may be incomplete

C:Superfamily: myosin heavy chain; myosin motor domain homology

C:Keywords: actin binding; ATP; coiled coil; hydrolase; methylated amino acid; muscle

F:89-76/Domain: myosin motor domain homology <MMOT>

F:179-186/Region: nucleotide-binding motif A (P-loop)

F:549-586/Region: actin binding #status predicted

F:656-678/Region: actin binding #status predicted

F:840-1940/Domain: coiled coil #status predicted <COI>

F:840-1280/Region: S2

F:181-1940/Region: light meromyosin

F:130/Modified site: N6,N6,N6-trimethyllysine (Lys) #status predicted

F:185/binding site: ATP (Lys) #status predicted

F:696,706/Active site: Cys #status predicted

Query Match 7.8%; Score 185.5; DB 1; Length 1940;  
Best Local Similarity 19.5%; Pred. No. 0.059;  
Matches 74; Conservative 84; Mismatches 180; Indels 41; Gaps 7;

OY 54 GKRTIKKLFPLDLOEENVL--LDAEFLKNEIDSVKAQLSQDKRKRDSQAIIIDTLRLPLE 112

Db 1262 GKNETORSLSLELTQKSRLOTETAGELSRQLEEKESIVSLSRSKQAFQOIEELRROLE 1321

OY 113 ERNATVESLONALNKAEMLCSTLKQKMFLEORODETQAREARLRCKMKMTMEQIELL 172

Db 1322 EENAKKALALALQSSRHDCDLRLQYEEEDGAELEQALSKANSVAQKRTYETDAI 1381

OY 173 -----LQSRSEVEEMIDMGVGSAAVEQLAVYCVSLK-----EYENLKRAKATGE 220

Db 1382 QRTLELEAKKIKLQRIQD--SEQVEAVNAKASLEKTKORLQGEVEDLMVDVERANS 1438

OY 221 LADLYKKDLYSSRSKLTNLTELDQAKLELSAOKDQADQETLSLRKSSDDPPGULEP 280

Db 1439 LAAALDKRQRFQVLAEMKTCESQAELEAALKEKRSSTLELFKLNAYEETLDLETL 1498

OY 281 ASATNETVSRLLVFESPAVEMNRLHOPRGDEIDLTFTFDVTPPTQTSQSGHCLPK- 339

Db 1499 VKRENKMLQEBISDLTMOISGKNLH-----LEKSRKQMELEKA 1539

OY 340 --KICLERARSPMONVLKRYKVKSPESQSLSGQRCVGEIDELAGAFPLFIRNAVIGQ 397

Db 1540 DIQALTEEAELAEHEBAKILRIQLTELTVQVSEIDRKIAEKDEIEQLKRYQRTV--E 1596

OY 398 KQPKRTTAESRSTDVARI 416

Db 1597 TMOGALDAEVRSRNEAIRL 1615

RESULT 13

A26655 myosin heavy chain [similarity] - slime mold (Dictyostellium discoideum)

N:Contains: myosin ATPase (EC 3.6.1.32)

C:Species: Dictyostellium discoideum



```

Query Match      7.6%: Score 182.5: DB 2: Length 501:
Best Local Similarity 22.0%: Pred. No. 0.018:
Matches 76: Conservative 78: Mismatches 141: Indels 51: Gaps 9:

Oy 68 QEEENVLDAEFLFNKLDYSKAOLSDREKRDQAIIITLRLPTLEERNATVESIONANLK 127
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 30 QNKQLRAMEDELMSSKDDYGVKNVHLEKSKRALBEOOVEEMKQLELEDELQATDADLR 89
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Oy 128 AEMLCSTLKQKMFLEQRDE-----TKQAREEAHRLKCKMK-----TMEQIEL 171
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 90 LEVNQAAMKAQEPERDLQARDEQSEEEKRLITFYQVRELFALEDEDKORALAVASKKMEI 149
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Oy 172 LLOSRSFEHEEIRDMGQGSABEOLAVYCVSLKREYENLRKARATGELADRLKKDLYS 231
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 150 DTKDEAQLEAANK---ARERRVKQLRRLQAMQKRYORELEBAKRSRDEIFAQSE----- 202
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Oy 232 SRSKSLKTINTELDAQKLELRSAOKDLOSADQETISLRKSDPPNLTLPASATNTVSR 291
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 203 SSKTKLSLEAELILQAELELASSERRARRHAEQERDEL---ADBIANSAGSKSLDEKRR 259
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Oy 292 -----VFESAPVPEMANPRLHQPPFGDEIDLNTTFDVNTPPTQTSQSHCLPK-- 339
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 260 EARMROLEEELEEEQSNMELLNDRFRK-----TTLQVDITNAELAEARSAAQSD 309
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Oy 340 --KLLEPARSPMGNVLTKKVHVKSKPESOLSLGS--QRCVGEIDDEL 382
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 310 NARQOLERONKDKAKLQLELGAVSKFRATISALEAKITQGLEEL 355

```

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RESULT 16
B70356
chromosome assembly protein homolog - Aquifex aeolicus
C:Species: Aquifex aeolicus
C:Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 02-Jun-2000
C:Accession: B70356
R:Deckerdt, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; O'
V.
Nature 392, 353-358, 1998
A:Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A:Reference number: A70300; MUID:98196666
A:Accession: B70356
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-1156 <AOF>
A:Cross-references: GB:AE000699; NID:g2983238; PIDN:AAC06839.1; PID:g2983243; GB:AE000699
A:Experimental source: strain VF5
C:Genetics:
A:Gene: xcpC
A:Superfamily: chromosome segregation protein SMC1

```

Query Match	7.6%	Score 181;	DB 2;	Length 1156;
Best Local Similarity	20.1%;	Pred. No. 0.055;		
Matches 81; Conservative	92;	Mismatches 141;	Indels 88;	Gaps 16;

```
OY      LAOEEN- ---LDAEFLKNELDSVKAQLSOKDRKRDQAIIID---TLRDIPEERNATE   119  
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :  
Db      LKEEREKLEKRELOIRIKRETFA - KILLKEEKLLIKEERILNELNLSRESTEDITTPIO  265  
  
OY      SLONAKNAEMLCSTLKKK-----KPLEORODETKQAREAHRLCKMKKTWEOIEL    171  
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :  
Db      ENEKELNERERLIKVENNEKIMPFKEKYVGFTAEIENARSRIKEKERELISENNRYNLDE  325  
  
OY      LLQSRSVEVEIMIRMGOGSAVEQLAVYCYSIKKEYENLEAKARATSELMDRLKKDVS    231  
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :  
Db      LINLLSLSKENIERVGTULOELEK-----LKEEYSLKEV-----                361  
  
OY      SRSKLKITNTTELDAQKL---ELRSAQKDLOSADOEITSLRKSDDPGNTLPASATN---  285  
||| : || : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :  
Db      EREKIRELEEERERKIIFDEVKKILEEEKELTEKLNLSNNEKOGL--EIQRANKNIIE     419  
  
OY      ETVASLVLESPPAV-----EMMNDRLHOPPGDEIDL-NTFEDVNTPPTOTSGSOH    335  
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
```

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Db 420 RINEDINKLIEREKEIKERKQELRLKAIKKKEEBELRNLQJLNIYEKR----- 473
QY 336 CLPKRLCLERARSPMONYLKVKHVKYKPSOLSIGORCGLDELAGAPLPIFIRAVL 395
Db 474 -----LSEYRKKEELKEELKGAIERVRSES-----DSDVDFKIDKGVGSV--SELI 519
QY 396 GOKOPNRTTAAESRSTDVYRIGFDGLGRTKFIOPRDTTIIR 437
Db 520 RYKNEPHITA-----LEVAG--GGRKKEIIVEDEEVAK 550

```

RESULT 17  
B43402  
myosin heavy chain-B, neuronal - chicken  
N:Contains: myosin ATPase (EC 3.6.1.32)  
C:Species: Gallus gallus (chicken)  
C:Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 19-Jan-2001  
C:Accession: B43402; A43402  
R:Takahashi, M.; Kawamoto, S.; Adelstein, R. S.  
J. Biol. Chem. 267, 17864-17871, 1992  
A:Title: Evidence for inserted sequences in the head region of nonmuscle myosin spectrin.  
myosin.

A:Accession: NB34402; MUID:92388144

A:Molecule type: mRNA

A:Residues: 1-2007 <RNA>

A:Cross-references: GB:MG3676; NID:g212448; PIDN:AAA4985.1; PID:g212452

A>Note: the sequence of residues 212-221 and 632-652 and the corresponding nucleotide

A:Accession: M43402

A:Molecule type: mRNA

A:Residues: 1-211;222-631;653-2007 <TA2>

A:Cross-references: GB:MG3676; NID:g212448; PIDN:AAA4985.1; PID:g212449

A>Note: sequence extracted from NCBI backbone (NCBI:112864)

C:Comment: Alternatively spliced segments 1 and 2 are found exclusively in nonmuscle

C:Superfamily: myosin heavy chain; myosin motor domain homology

C:Keywords: actin binding; alternative splicing; ATP; coiled coil; hydrolase; methyla

E:1-2007/Product: myosin heavy chain-B, neuronal #status predicted <MYN>

E:1-211;222-631;653-2007/Product: myosin heavy chain-B, nonmuscle #status predicted <

F:88-802/Domain: myosin motor domain homology <MMOT>

F:178-185/Region: nucleotide-binding motif A (P-loop)

F:212-221/Region: alternatively spliced segment 1 #status experimental

F:559-593/Region: actin binding #status predicted

F:632-652/Region: alternatively spliced segment 2 #status experimental

F:692-714/Region: actin binding #status predicted

F:875-2007/Domain: coiled coil #status predicted <COI>

F:875-1315/Region: S2

F:1316-2007/Region: light meromyosin

F:129/Modified site: NP, N6, N6-Crimethyllysine (Lys) #status predicted

F:184/Binding site: ATP (Lys) #status predicted

F:732,742/Active site: Cys #status predicted

F:1954/Binding site: phosphate (Thr) (covalent) #status predicted

F:1987/Binding site: phosphate (Ser) (covalent) #status predicted

Query match	7.68;	Score 181;	DB 1;	Length 2007;
-------------	-------	------------	-------	--------------

Best Local Similarity 21.5%; Pred. No. 0.1;  
Matches 96; Conservative 87; Mismatches 167; Indels 96; Gaps 16;

Qy	68	QEEENVNDAEFLKRLKELDSVYAAQLSQKDREKRSQALIIPTLROTLEERNNTVESLONALNK	127
Db	1536	QNKRLADRMEDLMSKSDYVKNNEHELEKSR-----TLEQVEEEMPTOLEBELDELOA	1586
Qy	128	AEMCSTFLKQMKPLEORODETQOAREPEARLEKCKM--KTMEIETLLLOSORSE-----	179
Db	1569	TEDAKLRLVNNQAMKQAFERDILQARDQONEEKKRRLVYQVRELEAELEDEKQKQALAVA	1648
Qy	180	----VEEMIRDMGVQ-----SAVEQLAVYCVSLKKEYENLKEARKATGELADRLK	226
Db	1649	AKKKEMDLMDL--EGQLEAANKARDEAIKQLRLQIQOMQDYQRELEAFARASDEIFAQSK	1707
Qy	227	KDLVSSSKSLKTLTLELDOAKKLELRSAQKDLOSADDEITSLLKKSSDPGPNLEPSSATNE	286
Db	1708	E-----SKRKLTGAEATLTLQDEFPASSERRRRRAEDOREL---ADELINSASGKSALLD	1760



QY 287 TVSR-----VFESAPVEMNPRLOPPGDEIDLTTEEDVNTPTPTSGSOHC 336  
 Db 1761 EKRLERAIADLEELDEESNMELNFRK-----TLQVTLNSELGERSA 1810  
 QY 337 LPKKLCERARSPMQLVKVH-KVSKPESQLSGGRCVGEDELDELACGAPFLTRNAV 395  
 Db 1811 AOKS---ENAHQOLERQKELKAKLOLEGSVSKFKATISTLEAKIKOL-----1857  
 QY 396 GOKPNTKRTASRSTDVYRIGFDGLGRTK-----FIQPRD-----TTIIRPVVSKA 445  
 Db 1858 -EDELDEAKERRAANKLVR-----RTEKLEVMQVEDERRHADQYKEQMEKANA 1908  
 QY 446 KSKOKVR-----IKTVSSASOPEL 464  
 Db 1909 RMKOLKROLEAEERATNANSRRKL 1934

RESULT 18  
 S02771

Myosin heavy chain A [similarity] - Caenorhabditis elegans  
 M:Contains: myosin ATPase (EC 3.6.1.32)  
 C:Species: Caenorhabditis elegans  
 C>Date: 31-Dec-1993 #sequence\_revision 19-May-2000 #text\_change 19-Jan-2001  
 C:Accession: T23622; S02771  
 R:Harris, B.  
 Submitted to the EMBL Data Library, August 1996  
 A:Reference number: Z19773  
 A:Accession: T23622  
 A:Status: translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-1992 <MIL>  
 A:Cross-references: EMBL:Z78199; PIDN:CA801576.1; GSPDB:GN00023; CESP:K12F2.1  
 R:Dbib, N.J.; Maruyama, I.N.; Krause, M.; Karn, J.  
 J. Mol. Biol. 205, 603-613, 1989  
 A:Title: Sequence analysis of the complete Caenorhabditis elegans myosin heavy chain gene  
 A:Reference number: S02771; MUID:89178677  
 A:Accession: S02771  
 A:Status: nucleic acid sequence not shown  
 A:Molecule type: DNA  
 A:Residues: 1-116,140-1992 <DIB>  
 A:Cross-references: EMBL:X08067; NID:96798; PIDN:CAA30856.1; PID:96799  
 C:Genetics:  
 A:Gene: myo-3; CESP:K12F2.1  
 A:Map position: 5  
 A:Insertions: 46/1; 192/1; 292/1; 468/2; 1921/3  
 C:Superfamily: myosin heavy chain; myosin motor domain homology  
 C:Keywords: actin binding; ATP; coiled coil; hydrolase; methylated amino acid; muscle cc  
 F:89-802/Domain: myosin motor domain homology <MMOT>  
 F:202-209/Region: nucleotide-binding motif A (P-loop)  
 F:680-712/Region: actin binding #status predicted  
 F:793-807/Region: actin binding #status predicted  
 F:875-1189/Domain: coiled coil #status predicted <COI>  
 F:875-1189/Region: S2  
 F:1190-1992/Region: light meromyosin  
 F:153/Modified site: N6,N6,N6-trimethyllysine (Lys) #status predicted  
 F:208/Binding site: ATP (Lys) #status predicted  
 F:730/740/Active site: Cys #status predicted

Query Match 7.5%; Score 180; DB 1; Length 1992;  
 Best Local Similarity 21.2%; Pred. No. 0.12;

Matches 126; Conservative 85; Mismatches 203; Indels 180; Gaps 24;

QY 31 LQCLIQWETAPSRTPCQRIQVCKTKTINKLFPDLAEEVNDLAEFLKNEKELDSVKAOL 90  
 Db 895 LEEAVQREIARSQLESQVADLVEEK---NALFSLFTEKANKLADAEERNEKTLNQLKATV 951  
 QY 91 SOK-----DREKRSQALIDP-----LRDTLEE---RNTV 118  
 Db 952 ESKSLDITGLEDQWERNEDLAROKKKTDOELSDPKKHVVQDELLESLRAAEDEKOSRDHNI 1011

QY 119 ESLQNALNKAEMLCSTLKQKKFLEORODETKQAREAHRLKCKMKTEQIELLOSORS 178  
 Db 1012 RSLQDEMANODEAVAKLNKEK---HQEESNRKLNDELQSEDEKVNHLKIRNKLBOQMD 1068  
 QY 179 EEEEM-----RDMGVGSAVEQLAVYC---VSLKEEYENL-----211  
 Db 1069 ELEENIDREKRSRGDIEKAKKRVGEGLKVQAQENIDETIKQKHADVETTLKREEDLHHTNA 1128  
 QY 212 -----KAKATGELADRLKLDVLS-----SNS-----KKTINTELDQ 245  
 Db 1129 KLAENNSIIAKLORLIKELTARMLELEERNSRQKSDRSREARELEELTERLEQ 1188  
 QY 246 -----AKEL-----RSAQKQDSADQEIYSLRKSDDPGNLEPASATNET 287  
 Db 1189 QCGATAQLEANKKREAIATLRKEKEDSLNHETATISLKRKHDSVAEL---TEQLET 1245  
 QY 288 VSRLEFESAPVEMNPRLOPPGDEIDLTNT-----TFDVNTPPTTSGSOH-- 335  
 Db 1246 LQKLAKSEAKSKLQORLDESSQAHATDSEVRSRODLEKALKTIEVQYSELQTKADEQSRQ 1305  
 QY 336 -----CLPKTL-----CLERARSPMQLVKVH-KVSKPESQLSGGRCVGEDELDEF-- 381  
 Db 1306 LQDFALKNRNLNNSDNLKSLLEEMDQNLNHLRLKSTLQSL-----DETRRNDEESRE 1361  
 QY 382 ---LAGAPLPFIRNAVVGOKQPNRTTAESRSPDVVR-----IGFDGLG-- 422  
 Db 1362 RQALAAATKAKNLEHENTYIIRE---HLDEAESKADLTQISKLNAEIQMKARPDSELN 1417  
 QY 423 -----GRTKFIQPR-----DTTIIRPVVSKAKSKQKVRKITYSSASOPEL 465  
 Db 1418 KLEIEAKKALQKLVQELTDTN-----EGLPAKIASQKQVRFKLMQDIDDAQSD 1467

RESULT 19

Myosin heavy chain nonmuscle form A - human  
 A:Alternate names: cellular myosin heavy chain; myosin type 9; NMHC-A  
 N:Contains: myosin ATPase (EC 3.6.1.32)  
 C:Species: Homo sapiens (man)  
 C>Date: 12-May-1994 #sequence\_revision 14-Jul-1994 #text\_change 19-Jan-2001  
 C:Accession: A61231; A34876; 152562; 161692  
 R:Simons, M.; Wang, M.; McBride, O.W.; Kawamoto, S.; Yamakawa, K.; Gdula, D.; Adelstein  
 Circ. Res. 69, 530-539, 1991  
 A:Title: Human nonmuscle myosin heavy chains are encoded by two genes located on diff  
 A:Reference number: A61231; MUID:91318083  
 A:Accession: A61231  
 A:Molecule type: mRNA  
 A:Residues: 1-715 <SIM>  
 A:Cross-references: GB:M69180; NID:g189029; PIDN:AAA61765.1; PID:g189030  
 R:Saez, C.G.; Myers, J.C.; Shows, T.B.; Reinwand, L.A.  
 Proc. Natl. Acad. Sci. U.S.A. 87, 1164-1168, 1990  
 A:Title: Human nonmuscle myosin heavy chain mRNA: generation of diversity through alt  
 A:Reference number: A34876; MUID:90138958  
 A:Accession: A34876  
 A:Molecule type: mRNA  
 A:Residues: 715-1961 <SAE>  
 A:Cross-references: GB:M1013; NID:g189035; PIDN:AAA36349.1; PID:g189036  
 R:Toothaker, L.E.; Gonzalez, D.A.; Tung, N.; Lemons, R.S.; Le Beau, M.M.; Arnaout, M.  
 Blood 78, 1826-1833, 1991  
 A:Title: Cellular myosin heavy chain in human leukocytes: isolation of 5' cDNA clones  
 A:Reference number: 152562; MUID:92003925  
 A:Accession: 152562  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-52, 'EAT', 56-659, 'T', 661-868, 'T', 870-930, 'C', 932-1239, 'KG', 1242-1337 <RE  
 A:Cross-references: GB:M8105; NID:g18988; PIDN:AAA59888.1; PID:g553596  
 R:Bement, W.M.; Hasson, T.; Wirth, J.A.; Cheney, R.E.; Mooseker, M.S.  
 Proc. Natl. Acad. Sci. U.S.A. 91, 6549-6553, 1994  
 A:Title: Identification and overlapping expression of multiple unconventional myosin  
 A:Reference number: A55758; MUID:94294418  
 A:Accession: 161692  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA

A:Residues: 182-218 <BEM>  
A:Cross-references: GB:I29141; NID:9457249; PIDN:AAA20904.1; PID:9531134  
C:Genetics:  
A:Gene: GDB:MYH9  
A:Cross-references: GDB:120216; OMIM:160775  
A:Map position: 22q12.3-22q13.1  
C:Superfamily: myosin heavy chain; myosin motor domain homology  
C:Keywords: actin binding; ATP; coiled coil; hydrolase; methylated amino acid; nucleotide  
F:84-764/Domain: myosin motor domain homology <MMOT>  
F:174-181/Region: nucleotide-binding motif A (P-loop)  
F:552-565/Region: actin binding #status predicted  
F:636-660/Region: actin binding #status predicted  
F:837-1938/Domain: coiled coil #status predicted <COI>  
F:837-1277/Domain: S2 #status predicted <DS2>  
F:1378-1961/Domain: light meromyosin #status predicted <LMM>  
F:1939-1961/Domain: carboxyl-terminal <CBT>  
F:125/Modified site: N6,N6,N6-trimethyllysine (Lys) #status predicted  
F:180/Binding site: ATP (Lys) #status predicted  
F:694/704/Active site: Cys #status predicted

Query Match 7.5% Score 179.5; DB 1; Length 1961;  
Best Local Similarity 19.2%; Pred. No. 0.12; Indels 161; Gaps 21;  
Matches 108; Conservative 113; Mismatches 181;

QY 48 QCRIVGKRTIKLFPDLQEEENV-----LDAEF--LKNELDSVKAQLSQK 93  
DB 1073 ELKQVLAKKE--EELQALAVVEEAQKNMALKKIRLEQISLEQLDSESRNRKA 1130  
QY 94 DREKRDGSAITDRLDLEERNATVESIQNALNKAEMCLSTLKK-----QNKLEIQ 144  
DB 1131 EKQKRDLEELAEALTELEDTLDSTAAQQLERSRKQEVNLIKLEEARKEHQIQDEM 1190  
QY 145 RQ-----DETQKAREHRLKCKM-----KTM-----QIELLQS-----QREEV 180  
DB 1191 RQKISQAVEELAEQLEQKRRKANLEKAKQTLLENRGELANENVKVLQGGHSEHKRRKV 1250  
QY 181 EEMIRDMGV-----GOSAVEQLAVYCVSLKKEYENLKEARKATGELADRLKDLVSSRSKL 236  
DB 1251 EAQQLQELQVKNRGEGRVTELDKVTKLQVELDNTGLQSDSKSSKLTGDFSALESQ 1310  
QY 237 K-----TLNTELDQAKLELRSAQKDLQSDADQ-----ITSL 267  
DB 1311 QDTQELQEEENRQKLSLSTKLQVEDEKNSFREOLEEEERAKHNLEKQIATLHAQVADM 1370  
QY 268 RKKSDDPGNLEPASATN-----ETYSRLVFESPA---PVEMMNPRLHQPPGDEIDL 317  
DB 1371 KKKMEDSVGLETAEYKRRKLQKDLGLISQHNHEEKVAAYDKLTKTRLQOELDLVDL 1430  
QY 318 N-----TTEDVNTPTQTSQSH-----CL 337  
DB 1431 DHQKQACNLEKKQKQKFDQLAAEETISAKYAEERDRAEAAREKETKALSLARALEEAM 1490  
QY 338 PKKICLERAA-----RSPQNVL-----KKYHKSKSPQSLSLGGQR---VGEIDELTA 383  
DB 1491 EQKLELELNKQFTFEMEDLSSKDDVGSVHLEKSKRALEQOVVEKKTKLELEDELQ 1550  
QY 384 GAFLEFLTNALVQKQKPRRTAESRSSTDVYRIGFDGLGRTKFLQPPDITIIIPV--PVK 442  
DB 1551 ATEPAKRLRY-----NLQMKAKQFERD-----LQGNDEOSEKKKQVLQVQVREME 1596  
QY 443 SKAKSKQKVRITKTVSSASQPKLD 465  
DB 1597 AELEDERKQRMAYAAARKKLEMD 1619

RESULT 20  
A59252  
myosin heavy chain, nonmuscle, form IIB - human  
N:Alternate names: myosin type 10; NMHC-B  
N:Contains: myosin ATPase (EC 3.6.1.32)  
C:Species: Homo sapiens (man)  
C:Date: 19-May-2000 #sequence\_revision 19-May-2000 #text\_change 02-Feb-2001

C:Accession: A59252; B61231; G02055  
R:Phillips, C.L.; Yamakawa, K.; Adelstein, R.S.  
J. Muscle Res. Cell. Motil. 16, 379-389, 1995  
A:Title: Cloning of the cDNA encoding human nonmuscle myosin heavy chain-B and analysis  
A:Reference number: A59252; MUID:96023307  
A:Accession: A59252  
A:Status: not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 1-1976 <SIM>  
A:Cross-references: GB:M69181; NID:g641957; PIDN:AAA99177.1; PID:g641958  
A:Experimental source: clone 11b lambda Zap II adult human T-cell library; cell line  
A:Note: Between nucleotides 1942-1943 in mRNA encoding human brain MHC-B there is an  
R:Simons, M.; Wang, M.; McBride, O.W.; Kawamoto, S.; Yamakawa, K.; Gdula, D.; Adelstein  
Circ. Res. 69, 530-539, 1991  
A:Title: Human nonmuscle myosin heavy chains are encoded by two genes located on diff  
A:Reference number: A61231; MUID:91316803  
A:Accession: B61231  
A:Molecule type: mRNA  
A:Residues: 63-237, 'K', 239-664, 'L', 666-722 <SI2>  
A:Cross-references: GB:M69181; NID:g641957  
R:Weir, L.  
submitted to the EMBL Data Library, August 1995  
A:Reference number: H00753  
A:Accession: G02055  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-81 <MEI>  
A:Cross-references: EMBL:U034304; NID:g1143217; PIDN:AAA84880.1; PID:g1143218  
C:Genetics:  
A:Gene: GDB:MYH10  
A:Cross-references: GDB:127350; GDB:G00-127-350; OMIM:160776  
A:Map position: 17p13-17p13  
C:Superfamily: myosin heavy chain; myosin motor domain homology  
C:Keywords: actin binding; ATP; coiled coil; hydrolase; methylated amino acid; nucleo  
F:88-771/Domain: myosin motor domain homology <MMOT>  
F:118-185/Region: nucleotide-binding motif A (P-loop)  
F:559-572/Region: actin binding #status predicted  
F:633-647/Region: actin binding #status predicted  
F:129/Modified site: N6,N6,N6-trimethyllysine (Lys) #status predicted  
F:184/Binding site: ATP (Lys) #status predicted  
F:701/711/Active site: Cys #status predicted

Query Match 7.5% Score 179.5; DB 2; Length 1976;  
Best Local Similarity 21.8%; Pred. No. 0.12;  
Matches 76; Conservative 77; Mismatches 140; Indels 55; Gaps 10;

QY 68 QEEENVDAEFLKNELDSSKAQLSQKDRKDSQAIDTLDLEERNATVESIQNALNK 127  
DB 1505 QNKQLRADMEDLMSSKDDVGNVHLEKSKRALQOQVEEMRTQLELEDELQATEDAKLR 1564  
QY 128 AEMICSTLKKQMKRLERODE-----TKQAREHRLKCKM-----TMEQIEL 171  
DB 1565 LEVNMQAKKQFERDLQTRDQNEKKRLLIKQVRELAELDERKQALAVASKKMEI 1624  
QY 172 LQOSQSEVE--EMIRDMGVGOSAVEQLAVYCVSLKKEYENLKEARKATGELADRLKDL 229  
DB 1625 DLKQLEAQIEAKNARD-----EVIKQLRKQAKQKQYQRELEAARARSROEIFQNSE-- 1677  
QY 230 VSSRSKTKLTNTELDQAKLELRSAQKDLQSDADQETSLRKSSDDPGNLEPASATNETVS 289  
DB 1678 --SEKKLKSLAEATILQOELASSERARRHAEQERDEL--ADEITNSASGKSLALDEKR 1732  
QY 290 RL-----VESPAPVDMNPRLHQPPGDEIDLNTFTVNTPTQTSQSHQLPK 339  
DB 1733 RLARIQAQLEEELEESQNNELMDLRFRK-----TTLQVDTLNAELAEARSAOK 1782  
QY 340 ----KICLERARSPQNVLLKVKHVSKEPSQSLGG--QRCVGEIDEL 382  
DB 1783 SDNARQOLEKONKELKAKLOELBGAVSKSRATISALEAKIGOLEED 1830

RESULT 21

PC4035  
cell-cycle-dependent 350k nuclear protein - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 08-Aug-1995 #sequence\_revision 19-Oct-1995 #text\_change 21-Jul-2000  
C:Accession: PC4035  
R:Li, Q.; Ke, Y.; Kapp, J.A.; Fertig, N.; Medsger Jr., T.A.; Joshi, H.C.  
Biochem. Biophys. Res. Commun. 212, 220-228, 1995  
A:Title: A novel cell-cycle-dependent 350-kDa nuclear protein: C-terminal domain sufficient for cell cycle arrest  
A:Reference number: PC4035; MUID:95336446  
A:Accession: PC4035  
A:Molecule type: DNA  
A:Residues: 1-1017 <L10>  
A:Cross-references: GB:Q25725; NID:g918866; PIND:AAA86889.1; PID:g918867  
A:Note: Repeat 15-160 and 200-340  
C:Comment: This protein contains a coiled-coil and a globular domain at the carboxy-terminus  
C:Keywords: nucleoprotein; phosphoprotein  
E:835/Binding site: phosphate (Thr) (covalent) (by calmodulin-dependent kinase II) #status F:825,826,838/Binding site: phosphate (Ser) (covalent) (by cAMP-dependent kinase) #status F:908,909/Binding site: phosphate (Thr) (covalent) (by cAMP-dependent kinase) #status

Query Match	7.5%;	Score	179;	DB	2;	Length	1017;
Best Local	Similarly	21.6%;	Pred.	No.	0.061;		
Matches	86;	Conservative	69;	Mismatches	159;	Indels	84;
						Gaps	9;

Qy	56	KTIIINKJFFDLAJOEEN----	VILAEFLKNEISVKAOLSO	OKDERKDSQAIIIDL	BDTL	11.1
Db	56	KDKVENERELQJSEENOEOLYI	DAENSKAEVETLQIEEMARSL	VEFLDVTIRSEK	11.5	
Qy	112	EEBNATVESLONALNKAEMLCS	TLKKOMKPLEQRO-----			14.6
Db	116	ENLTKQIOEKGGQJSELDKIL	SKSQJLEKEQAIEIQIESKTA	YVEMLOJQNKELNEAV	17.5	
Qy	147	-----	DETKQAREAHRLCKMKMTME	QJELLLOSORSE-----		17.9
Db	176	AALCGDEIMKATEOSLDPR	IEEHOJLRNJSIEKRLARLE	DEDEKKQJCVLQOLKESE	HNAD	23.5
Qy	180	-----	VEEMIDMGVGGSVAVQJLAV	CVJSUKKEVENIKERKATG	ELADLKKDLYSSR	23.4
Db	236	LLKGRVENLERELEIARTNO	HALEBENSUGEVELIKAKI	EGTQJOSLRGLJELDVY	TI RS	29.5
Qy	235	KLKTINTFLDQ-----	AKLEL--RSAQKDLOS	AOEFTLSLRKKSDDP	PGNL-----	27.8
Db	296	EKEDTINLOJKEQERISLE	LIINSFENIIOEKQEKVOM	KEKSTAMEMLOJLKS	MSMR	35.5
Qy	279	--EPASATNETVSRLVESP	APVEMMNPRLHQPPFG--	DEIDLN--	TTFDVNTPPQJTSG	33.2
Db	356	EMOPCIMTKRPSVAKEO	NJLSOVCECTELEKQJL	LOGDEAKNNYIVLOSS	NGLIQVED	41.5
Qy	333	SOHCJPKK--LCLEBARSP	MOVAVLKKVHKVS	PPESQJLS	36.9	
Db	416	GKQJLEKKEDEISIRKNO	IOEOJLVSQJVEEHOJL	45.3		

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RESULT 22
S21801
myosin heavy chain, neuronal [similarity] - rat
N:Alternate names: myosin II
N:Contains: myosin ATPase (EC 3.6.1.32)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 19-Jan-2001
C:Accession: S21801; P00013; S18134
R:Sun, W.; Chantler, P.D.
J. Mol. Biol. 224, 1185-1193, 1992
A:Title: Cloning of the cDNA encoding a neuronal myosin heavy chain from mammalian brain
A:Reference number: S21801; MUID:92235856
A:Accession: S21801
A:Molecule type: mRNA
A:Residues: 1-1999 <SUN>
A:Cross-references: EMBL:X62659
R:Sun, W.; Chantler, P.D.
Biochem. Biophys. Res. Commun. 175, 244-249, 1991
A:Title: A unique cellular myosin II exhibiting differential expression in the cerebral

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A:Reference number: PNM013; MUID:91151356  
A:Accession: PNM013  
A:Molecule type: mRNA  
A:Residues: 1914-1998, 'I' <SU2>  
A:Experimental source: brain  
C:Superfamily: myosin heavy chain; myosin motor domain homology  
C:Keywords: actin binding; ATP: coiled coil; hydrolyase; methylated amino acid; nucleoside  
F:84-763/Domain: myosin motor domain homology <MMOT>  
F:174-181/Region: nucleotide-binding motif A (P-loop)  
F:541-575/Region: actin binding #status predicted  
F:653-675/Region: actin binding #status predicted  
F:836-1999/Domain: coiled coil #status predicted <COI>  
F:836-1276/Region: S2  
F:1277-1999/Region: light meromyosin  
F:125/Modified site: N6,N6,N6-trimethyllysine (lys) #status predicted  
F:180/Binding site: ATP (lys) #status predicted  
F:693,703/Active site: Cys #status predicted  
F:1916/Binding site: phosphate (Ser) (covalent) #status predicted  
F:1943/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match	7.5%	Score 178.5	DB 1	Length 1999
Best Local Similarity	20.9%	Pred. No. 0.14		
Matches 93	Conservative 81	Mismatches 153	Indels 117	Gaps 15

Query Match	7.5%;	Score 178.5;	DB 1;	Length 1999;
Best Local Similarity	20.9%;	Pred. No. 0.14;		
Matches	93;	Conservative 81;	Mismatches 153;	Indels 117;
				Gaps 15;

QY	48	OCRIOWGKTIINKLFPFDLQOEENV-----	-IDAEF--	-LKNELDSVTKQJLSOK	93
Db	1072	ELKQJWLAKK--	-BELQALALRVEEBAQAOKMALKKITRELESQISOLEDBEDLESERSRNKA	11293	
QY	94	DREKRDQAIDTLDRDLREERNATVESIQNALNKAAMLCSITLK-----	-QMKFLQD	144	
Db	1130	EKOKRDLEGEELAEKLTETEDLTSTAAQOGLRSKRDQEVNIIKLKLTDEEAKTHQAQIEM	1189		
QY	145	RODEKQAREBAHL-----	-KKCKMTM-----	-QIELLQS-----	QREY 180
Db	1190	ROKSHQAVEELAEBOLEOTKRRVNALEKAKOTLENERGELANEKVVLLQGRDSEHKRRKV	1249		
QY	181	EEIMIDMGV--	-QASAVEQILAVYCSILKKEYENLEKARKATGELADRYLKCVSSRSK	236	
Db	1250	EAQOLOELOVKNBEERBRVTELADKVTKQJVELDNYTGILSQSDSKSKSLTKTRFSAJLEQL	1309		
QY	237	K-----	-TNTELDAQKTELNSAQOLOQADQ-----	-ITSL	267
Db	1310	QDTOLLEOENRQKLSITKLQYEDSEKNSFRQULEEEEBEBAKNHLEKOIATLHQAQVDM	1369		
QY	268	RKSSDDPRGNLEPASAAN-----	-ETVSVLYPEEA--	-PACMMNPRJHORPPCEIDL	317
Db	1370	KKKMEDSVGCLTEAEVVKRKLOKDLBESLQRHEEKYAANDKLEKTKYTRLOQOELDLQVLDL	1423		
QY	318	N-----	-TTEDVNTPTQTSQONCLPKKLCLEERAKSPQONVILKVVHVRKSP	364	
Db	1430	DHQRASACNEKKOKFPD-----	-QLLAEITKSAKYAEERBARDADEERAETKATKTELJAR	1483	
QY	365	SOLSLGQGR-----	-VGLDEEL	382	
Db	1484	AELAMEQKAELFKRNQIEMTERI	1507		

RESULT 23

S67593

transport protein USO1 - yeast (*Saccharomyces cerevisiae*)

N.Alternate names: protein D2552; protein YDI058W

C.Species: *Saccharomyces cerevisiae*

C.Date: 12-Jul-1996 #sequence\_revision 12-Jul-1996 #text\_change 21-Jul-2000

C.Accession: S67593; A38455; S30782

R.Bioecker, H.; Brandt, P.

submitted to the Protein Sequence Database, July 1996

A.Reference number: S67587

A.Accession: S67593

A.Molecule type: DNA

A.Residues: 1-1790 <BLO>

A.Cross-references: EMBL:Z74106; NID:q1431058; PID:e253003; PID:q1431059; MIPS:YDI058W

A.Experimental source: strain 5288C

R:Nakajima, H.; Hirata, A.; Ogawa, Y.; Yonehara, T.; Yoda, K.; Yamasaki, M.  
 J. Cell Biol. 113, 245-260, 1991  
 A:Title: A cytoskeleton-related gene, USO1, is required for intracellular protein transp  
 A:Reference number: A38455; MUID:91185402  
 A:Accession: A38455  
 A:Molecule type: DNA  
 A:Residues: 1-389, 'TA', 392-724, 'S', 726-1790 <NAK>  
 A:Cross-references: GB:X54378; NID:94777; PIDN:CA38253.1; PID:94778  
 A:Note: the authors translated the codon ACT for residue 768 as Ile  
 R:Hostetter, M.K.; Herman, D.J.; Bendel, C.M.; McClellan, M.; Tao, N.; Kendrick, K.E.  
 submitted to the EMBL Data Library, February 1993  
 A:Description: An integrin analogue in Saccharomyces cerevisiae.  
 A:Reference number: S30782  
 A:Accession: S30782  
 A:Molecule type: DNA  
 A:Residues: 71-846, 'E', 848-923, 'K', 925-1252, 'I', 1254-1318, 'V', 1320-1460, 'S', 1462-1580, 'S  
 A:Cross-references: EMBL:L03186  
 C:Genetics:  
 A:Gene: SGD:USO1; INT1  
 A:Cross-references: SGD:S0002216; MIPS:YDL058w  
 A:Map position: 4L  
 C:Keywords: coiled coil; transmembrane protein  
 F:326-342/Domain: transmembrane #status predicted <TM1>  
 F:394-410/Domain: transmembrane #status predicted <TM2>  
 F:617-633/Domain: transmembrane #status predicted <TM3>

Query Match 7.4%; Score 178; DB 2; Length 1790;

Best Local Similarity 18.1%; Pred. No. 0.13; Mismatches 177; Indels 80; Gaps 13;

Matches 81; Conservative 110; Mismatches 177; Indels 80; Gaps 13;

QY 56 KTIINKLFEDLAQEEENVLDA-EFLKNE---LDSVKAQLSQDKREKRQSAIIDTLRDT 110  
 Db 965 KSLANN-YKDMAENESEILKAVEESKNESISQLSNLQNKIDSMQEKNFQIERSIEKN 1023  
 QY 111 LEERATVESIQNA---LNKAEMLCSTLKQMKFLERODTKQAREE-AHRLCKMKMT 165  
 Db 1024 IEQLKRTISDLEQTKKEETISKSDSKDEYESQISLKEKLEFATYANDEMNKISLTKT 1083  
 QY 166 MEQIELLOSOREVEEMIRDMVGQSAVEOLAVYCVSLKKEYENLKEARKATGELADRL 225  
 Db 1084 REELAEELAAKYNLKNLETKLETSEKAIKE-----VKNEEHLEKKEIOLEKATET 1136  
 QY 226 KDLVSSRSKLTTLTTELDOAKLELRSQK-----DLASADOETLSL 267  
 Db 1137 KOQLNSLRANLESLKEHEHDLAAQLKKEEQANKEROYNEEISQLNDEITSTQGENESI 1196  
 QY 268 RKSSDPPGNLEPASATMETVSRVLFESPAPYEMNNPRLHQPFEGDEIDLTTFDVTNPP 327  
 Db 1197 KKKNDLEGEYKAMKSTSEOSNL---KKSEIDLALNLIKE----- 1234  
 QY 328 TQTSQSHCLPFPKICLLEFAR--SPMQNYLKKVKVSKPESQSLSGORCVGELDEELAGA 385  
 Db 1235 -----LKKKNTNNAASLLESIKSYSEVTKIKELQDECNF-KEKEVSELEKLAAS 1284  
 QY 386 PPLFRANAVLGOKQPNRTTAESRSSTDVVRIGFDGLGRTKFIQPRDTTIIIRPVVKSK- 444  
 Db 1285 EDKNSKYLEL-QKESEKIKEELDAKTTELKQIKITNLKSKAKESSESLSKTKTSSE 1343  
 QY 445 -----AKGKQVRIKTVSSASQPKL 464  
 Db 1344 RKNMEQLEKLKNEIQKNQAFEKERKL 1371

# RESULT 24

T38077  
 hypothetical coiled-coil protein - fission yeast (Schizosaccharomyces pombe)  
 C:Species: Schizosaccharomyces pombe  
 C:Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 03-Dec-1999  
 C:Accession: T38077  
 R:Connor, R.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.  
 submitted to the EMBL Data Library, April 1996  
 A:Reference number: 221767

A:Accession: T38077  
 A:Status: preliminary; translated from GR/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-1957 <CON>  
 A:Cross-references: EMBL:Z70690; PIDN:CA94624.1; GSPDB:GN00066; SPDB:SPAC1F3.06c  
 A:Experimental source: strain 972h-; cosmid c1F3  
 C:Genetics:  
 A:Gene: SPDB:SPAC1F3.06c  
 A:Map position: 1

Query Match 7.4%; Score 177.5; DB 2; Length 1957;

Best Local Similarity 20.6%; Pred. No. 0.15;

Matches 74; Conservative 70; Mismatches 135; Indels 81; Gaps 9;

QY 70 EENVDAEFKINLELVKNAQLSQDKREKRQSAIIDTLRDLTEERNATVESIQNLNKA 129  
 Db 1386 EDNQLATYKLNQDLHNLQEDVLEKESLITLSEESLSNOROKESSLDAKNELE 1445  
 QY 130 -MLCSTLKQMKFLERDQ-----DETQAREEAHRLCKMKTMEQIELLOSOREVE 181  
 Db 1446 HMLDTSRKNSSLMKESINSISLDDKSFELASAVKELGALQKLSSELSMENIKSOLQ 1505  
 QY 182 EMIRDMVGQSAVEOLAVYCVSLKKEYEN-----LKEARKATG 219  
 Db 1506 EAKERIQVDESTIOELDEHETASKNNYEGKLNDKDSIIRDSENIEQNLNLAEKSAVK 1565  
 QY 220 ELADLKKDIVSSRSKLTTL-----NPELDOAKLELRSQKQDSADQDETSLRKSD 272  
 Db 1566 RISTEKESLIQPNRLDLLEYHNKSQVSELSRSLKSLATTEELQLENEKSLTTTML 1625  
 QY 273 DPGNLEPASATMETVSRVLFESPAPYEMNNPRLHQPFEGDEIDLTTFDVTNPPQTSG 332  
 Db 1626 DLQNVKQLSNIKDLSL-----DLRTLRSL-DSVASL 1658  
 QY 333 SOHCLPKKLCLEPARSPMQNYLKKVH-----KVSPPESQSLSGORCVGELDEELAG 384  
 Db 1659 QKECKIKSNVVE---SLQDVLTYSQVARNAELEDEVSRVDIRRRDRCC-----EHLSG 1709

# RESULT 25

T30171  
 ninein - mouse  
 C:Species: Mus musculus (house mouse)  
 C:Date: 22-Oct-1999 #sequence\_revision 22-Oct-1999 #text\_change 22-Oct-1999  
 C:Accession: T30171  
 R:Bouckson-Castaing, V.; Moudjou, M.; Ferguson, D.J.P.; Mucklow, M.; Belkaid, Y.; M11  
 J. Cell Sci. 109, 179-190, 1996  
 A:Title: Molecular characterisation of ninein, a new coiled-coil protein of the centr  
 A:Reference number: 220751; MUID:96431720  
 A:Accession: T30171  
 A:Status: preliminary; translated from GR/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-2168 <BOU>  
 A:Cross-references: EMBL:U40342; NID:9113864; PID:9113865; PIDN:AAA83234.1  
 A:Experimental source: Strain C57BL/6  
 A:Note: localised specifically in the pericentriolar matrix of the centrosome

Query Match 7.4%; Score 177; DB 2; Length 2168;

Best Local Similarity 21.3%; Pred. No. 0.18;

Matches 105; Conservative 83; Mismatches 174; Indels 130; Gaps 21;

QY 31 LOCLQWFEIAPSRCPQCRIOVGKTIINKLFPDLAQEEENVDAEFLK-NELDSV--- 86  
 Db 1515 LKAMWQ-----PAVTCGEMQ-----RKVELLRESEKLOEENSILKNETITLNEEDSISNL 1565  
 QY 87 -----KAQLSQK-----DREKRQSAIIDTLR---DTLEERNATVE-----SIQNAL 125  
 Db 1566 KLEELNGSQBELMKIETIIRBEKASIQIYWEKIKQVSDLKIKNQDLSENLKSKNSQ 1625  
 QY 126 NK-----AEMLC-----STLKKQK-KFLERQDETQKAREEAAH 157

Db 1626 NKEELKTLNORLAEMLCOREPACCTSEKWEQENASLKEELDHKKVOTSLVSSLEAEIS 1685  
 QY 158 RLKCKMTMEIOIELLOSOREVEEMIR---DMGQSAVEOLAVYCSIKKEVE----- 209  
 Db 1686 RIKLQTHMEQENLLKDELRLKQHLRCPDLSLQOKMSSVLSYNEKLKEKVLSEEL 1745  
 QY 210 -----NLEKARKATGELADRLKDLVSSRSKLTLTNTELDQAKLELR 251  
 Db 1746 KSCADKLAESSLLEHRTATKQEQETAMEEQESLSQLAASQAQVQDELDVQVNVNQMA 1805  
 QY 252 SAQKDLO-----SADQETSLRKK-----SDDPGNEPASAINEVS----- 289  
 Db 1806 EIESDLQVTRQEKRAVQEWMSLHRQLNADIKDMVSEETAP-HISGLRGQORRLSMDKLD 1864  
 QY 290 RLVEESPAPYEMNPRHLQHPPEFGDEIDLNTT-----FDVTPPT--QTSSQCHLPRKL 341  
 Db 1865 HLMNEEPOLLQOESKRKLQTVVQNTQADLTJHSREKRVQLESNLTPTKHOKQLNQPCTVKS- 1923  
 QY 342 CLERARSPMNVLTKKVHKVPESQSLSGQRCVGELEDELACAPPLFIRNAVIGOK--Q 399  
 Db 1924 -TEQEKLTIRCEQSQKESQSPIS-----RKYGQMSGLERGLTHTLENEGKTKKQMQ 1975  
 QY 400 PNRTAESRSST 411  
 Db 1976 PLRSTVTRSPSS 1987

RESULT 26  
 A27224  
 myosin heavy chain II - Acanthamoeba castellanii  
 N:Contains: myosin ATPase (EC 3.6.1.32)  
 C:Species: Acanthamoeba castellanii  
 C>Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 19-Jan-2001  
 C:Accession: A27224  
 R:Hammer III, J.A.; Bowers, B.; Paterson, B.M.; Korn, E.D.  
 J. Cell Biol. 105, 913-925, 1987  
 A:Title: Complete nucleotide sequence and deduced polypeptide sequence of a nonmuscle my  
 A:Reference number: A27224; MUID:87308395  
 A:Accession: A27224  
 A:Molecule type: DNA  
 A:Residues: 1-1509 <HAM>  
 A:Cross-references: GB:Y00624; GB:M12702; GB:M12703; GB:M19549; NID:95585; PIDN:CAAG6663  
 C:Genetics:  
 A:Introns: 69/3; 119/3; 181/2  
 C:Superfamily: myosin heavy chain; myosin motor domain homology  
 C:Keywords: actin binding; ATP; coiled coil; hydrolase; methylated amino acid; nucleotide  
 F:92-775/Domain: myosin motor domain homology <MOT>  
 F:182-189/Region: nucleotide-binding motif A (P-loop)  
 F:544-576/Region: actin binding #status predicted  
 F:660-682/Region: actin binding #status predicted  
 F:848-1227/Domain: coiled coil #status predicted <COI>  
 F:1228-1247/Domain: hinge <HIN>  
 F:1448-1482/Domain: coiled coil #status predicted <CO2>  
 F:1483-1509/Domain: carboxyl-terminal <CBT>  
 F:133/Modified site: N6, N6, N6-trimethyllysine (Lys) #status predicted  
 F:188/Binding site: ATP (Lys) #status predicted

Query Match 7.4%; Score 176.5; DB 1; Length 1509;  
 Best Local Similarity 24.5%; Pred. No. 0.13;  
 Matches 81; Conservative 63; Mismatches 113; Indels 73; Gaps 15;  
 Db 66 LAOEENVLDAEFLKNELDSVKAQLSQKDRKDSQAIIIDRLRLTERNA-----TVESL 121  
 QY 888 LAEE-----DADKLEKDLAALKLILDLGSKAD-----LEEDNALQKRVAGL 931  
 Db 122 QNALKAEMLCSTLKKQMFLEORODETKQAREFAHRLCKMKMTMEQIELLOSORESEVE 181  
 QY 932 EEELOEERSASNDILEQKRKLEAEKGLKASLEEBER---NRKALQEKATVESERNLQ 988  
 Db 182 EMIRMGVGSQAVEOLAVYCSLKKEYENL-KEARKATGELAD--RLKKDLVSSRSKLT 238  
 QY 989 DKYEDEAAHD-----SLKKKEBDLSRELRETQDALADAEINISETL---RSKIKN 1035

QY 239 -----LNTLEDO---AKLELSAOKDLSADOETSLRKKSDPPGNEPASAINEV 288  
 Db 1036 TERGADVRYNELDDVYATKTLQLEKTKSL--BEELQOTRAOLEEESKGEAASSRAKOL 1092  
 QY 289 SRLVESAPYEMNPRHLQHPPEFGDEIDLNTTQDVNTPTQTSQCHLPRKLCLERARS 348  
 Db 1093 GQQLDARSEVDSLKSLTS-----AAKSLTKVAKQNNDLDEQ-----LEDERT 1136  
 QY 349 PMONVLTKKVH---KVSPPESQL-SLGGOR 373  
 Db 1137 VRANVDKQKALEKAKLTLELDQVYALDQK 1166

RESULT 27  
 T16270  
 hypothetical protein F35D11.1 - Caenorhabditis elegans  
 C:Species: Caenorhabditis elegans  
 C>Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 20-Sep-1999  
 C:Accession: T16270  
 R:Fullon, B.  
 Submitted to the EMBL Data Library, June 1995  
 A:Description: The sequence of C. elegans cosmid F35D11.  
 A:Reference number: Z18487  
 A:Accession: T16270  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-1827 <FUL>  
 A:Cross-references: EMBL:U29381; NID:9868214; PID:9868224; PIDN:AAA68757.1; CESP:F35D  
 A:Experimental source: strain Bristol N2  
 C:Genetics:  
 A:Gene: CESP:F35D11.11  
 A:Introns: 76/2; 131/3; 185/3; 221/3; 253/3; 320/1; 869/3; 1133/3; 1205/2; 125

Query Match 7.4%; Score 176.5; DB 2; Length 1827;  
 Best Local Similarity 25.3%; Pred. No. 0.16;  
 Matches 61; Conservative 63; Mismatches 82; Indels 35; Gaps 9;

QY 52 QVQKKT---IINKLFPDLAEOEENVD-----AEFLKNELDSVKAQLSQKDRKRD 99  
 Db 657 QVNERTRQISEANKKYDDAARKNDALLDEVATWQEKYEQLMKLEEMNRGQEKEREERAD 716  
 QY 100 SQATIIDLTR-----DTLEERNATVESLQNALKKAEMLCSTLKKM-KPLEORODETKQ 151  
 Db 717 LRALLDIDRGNFDKLTNELKQGVTVDSLANEI-----SLKEQLKSEKEREKEELR 769  
 QY 152 AREFAHRLCKMKMTMEQIEL-LLOSORESEVEEMIRDMGQSAVEOLAVYCSLKKEYEN 210  
 Db 770 MEELQKNEMAKREVEYKQLQAEKDGQGVENFQKEC---EARNNELTKIHEMLMEERHD 826  
 QY 211 LKEARKATGELADRLKDLVSSRSKLTLTNTELDQAKLELSAOKDLSQADQF-ITSLRK 269  
 Db 827 LKVQHLHTEEEVERLKEKM--RKLEKLNQNDGDRAEWSENRNRLSSKNEAVTELQ 883  
 QY 270 K 270  
 Db 884 R 884

RESULT 28  
 B44972  
 paramyosin - nematode (Onchocerca volvulus) (fragments)  
 C:Species: Onchocerca volvulus  
 C>Date: 14-May-1993 #sequence\_revision 14-May-1993 #text\_change 02-Jul-1998  
 C:Accession: B44972  
 R:Limberger, R.J.; McReynolds, L.A.  
 Mol. Biochem. Parasitol. 38, 271-280, 1990  
 A:Title: Filarial paramyosin: cDNA sequences from Dirofilaria immitis and Onchocerca  
 A:Reference number: B44972; MUID:90220759  
 A:Accession: B44972  
 A:Status: preliminary  
 A:Molecule type: mRNA









R;Seelig, H.P.; Schranz, P.; Schroeter, H.; Wiemann, C.; Griffiths, G.; Renz, M.  
Mol. Cell. Biol. 14, 2564-2576, 1994  
A:Title: Molecular genetic analyses of a 376-kilodalton Golgi complex membrane protein  
A:Reference number: A56539; MUID:94187728  
A:Accession: A56539  
A:Molecule type: mRNA  
A:Residues: 1-3259 <SEE>  
A:Cross-references: EMBL:X75304; NID:9405714; PIDN:CA53052.1; PID:9405715  
C:Genetics:  
A:Gene: GDB:GOLGB1; GCP: GCP371  
A:Cross-references: GDB:454958  
A:Map position: 3q13.31-3q13.31  
C:Superfamily: giantin  
C:Keywords: coiled coil; Golgi apparatus; transmembrane protein  
F:3338-3254/Domain: transmembrane #status predicted <TM>

Query Match 7.3%; Score 174.5; DB 1; Length 3259;  
Best Local Similarity 21.1%; Pred. No. 0.39;  
Matches 115; Conservative 88; Mismatches 174; Indels 169; Gaps 20;

QY 30 HLOCLIMFE-----TAPSTPCQCRIOYGGKTIINKLFEDLAQEEENLDA--- 76  
DB 720 NLNQLIEFKKNADNNSAFTALSEERDQLLSQYKELSMVETLRAQYKOLEMNLAEAEQ 779  
QY 77 -----EFLKNELDSVKAOLSOXKREKRDSQAI 103  
DB 780 RLIDYESOTAHNDLTLTEQIHSLTEAKSKDYKITEVLONEDDVLQDSQETLIRLSQSQ 839  
QY 104 IDTLR-DTLE--ER---NATESLONLANKAEM-----LCSTLKKOMKFLERODET 149  
DB 840 LONKESELEGAERHVRHISKEVELSOLSQELEITRMQDLLEKKRDVETLQOTTEK 899  
QY 150 K-----QAREAHRLKCKMKTM-BOIELLLOSQSEVEEMIRDMGV---- 189  
DB 900 DQVTEISFSKTEKRVOLNEKEFSLGVEIKTLKEQLNLHSAEBAKKEQVEDNEVSSGL 959  
QY 190 -----GOSAVEOLAVYCVSLKKEYEENLKEA-----RKATGELADLKKDLVSS 232  
DB 960 KQNDENSPAGQISKEELQHFEDLKKENBQRKKLQALINKRELLQVRSLEBELANL 1019  
QY 233 RSKLKT-----LWTELDQAKLELRSQKD 256  
DB 1020 KDECKEILPSETERGEVEEDKENKEYSEKCVTSKCEIEIYLKQTISEKEVELOHNRKD 1079  
QY 257 LQ----SADQETLSLRKSDDPGNLERSATNTEVSRVFPSPAVEMNRLQPPGCD 313  
DB 1080 LEKRLAEEOFOALVKQWNO---TLQDKTQIDLLQAEISENOALIQKLITSNTDASDGD 1136  
QY 314 EIDNLTFTDVNTPTQTSGSOHCLP---KKLCLEARRSPQWNLKK-----VHKVS 361  
DB 1137 SVALLVEKVVISPPC-TGSSSHMKRPELEKTLAEKEKEQLOKLOELVTSRKALLKKAQ 1195  
QY 362 KPESOL-SLGGQ-----RCVGELEDE-----ELAGAPLFTIRNAVILQOKPNRTTA 405  
DB 1196 EKENHLEELKQKDDYRRLQEOFDQSKENENIGDQLRQIQVRESIDQ-KLPSTFQQ 1254  
QY 406 ESRST 411  
DB 1255 ESCRST 1260

RESULT 36  
S00084  
myosin heavy chain, fast skeletal muscle - rabbit (fragment)  
C:Species: Oryctolagus cuniculus (domestic rabbit)  
C:Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 20-Jun-2000  
C:Accession: S00084; S14807  
R;Mada, K.; Sczakiel, G.; Wittlinghofer, A.  
Eur. J. Biochem. 167, 97-107, 1987  
A:Title: Characterization of cDNA coding for the complete light meromyosin portion of a  
A:Reference number: S00084; MUID:87304245  
A:Accession: S00084

A:Molecule type: mRNA  
A:Residues: 1-676 <MAE>  
A:Cross-references: EMBL:X05958; NID:91622; PIDN:CAA29391.1; PID:91364242  
A:Note: the sequence from Fig. 5 is inconsistent with that from Fig. 3 in having 561-  
R;Mada, K.; Roesch, A.; Mada, Y.; Kaldtzer, H.R.; Wittlinghofer, A.  
FEBS Lett. 281, 23-26, 1991  
A:Title: Rabbit skeletal muscle myosin. Unfolded carboxyl-terminus and its role in mo  
A:Reference number: S14807; MUID:91200294  
A:Accession: S14807  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 668-676 <MA2>  
C:Superfamily: myosin heavy chain; myosin motor domain homology  
C:Keywords: actin binding; ATP; coiled coil; muscle; skeletal muscle  
F:21-676/Domain: light meromyosin <LME>

Query Match 7.3%; Score 174; DB 2; Length 676;  
Best Local Similarity 20.8%; Pred. No. 0.069;  
Matches 80; Conservative 81; Mismatches 157; Indels 66; Gaps 13;

QY 68 QEENNVDAEFLKELDSVA-----QLSQND-----REKRDSQAI---IDTLRD 109  
DB 3 KEEEH---ORLINELSAQRARLHTESGERSRQDEKDAWVSQLSRGQAFTQOIEGLKR 58  
QY 110 TLEERNATVESLONLANKAEMLCSTLKKOMKFLERODETQAREEAH-----RLCKM 163  
DB 59 QLEETAKSALAHALOSSRRDCDLREQYEEDEKAELQRAMSKANSEYQRTGCET 118  
QY 164 KTMBOIELLLOSQSEVEEMIRDMGVGOSAVEOLAVYCVSLKKEYEENLKEARKATGELAD 223  
DB 119 DAIO RTE-ELEBAKKLQARLOD---AEHVEAVNSKASILEKTKRQLO--NEAEDLMID 172  
QY 224 RLKDLVSSRKLTMTLNT-----LDAQLELSAQKDLQSAQDETSLRKSDDP 274  
DB 173 VERSNATCARDKQRNFQVLAEMKHYEFTQALASQESRSLSSTEFVKVNAVEES 232  
QY 275 PGNLEPASATNTEVSRVFPSPAVEMNRLHQ-PPFGDIDNLTFTDVNTPTQTSGS 333  
DB 233 LDHLETLKREKNLQOETSLDTEQIAESAKIHILEYKKQID----- 275  
QY 334 QHCLPRKLCLEARRSPQWNLKVKVSKPESQLSGQRCVGLDELAGAPLFTIRNA 393  
DB 276 QEKSELQALAEAGSLSEHGEKGLIRIQLELQYKSEIDRIAKKDEI-----DQLRKH 331  
QY 394 V-LGQKQPNRTTAERSSTDVRI 416  
DB 332 LRVEVMSQSTLDAEIRSRNDALRI 355

RESULT 37  
B55094  
chromosomal protein XCAP-E - African clawed frog  
C:Species: Xenopus laevis (African clawed frog)  
C:Date: 23-Mar-1995 #sequence\_revision 05-Apr-1995 #text\_change 02-Jun-2000  
C:Accession: B55094  
R;Hirano, T.; Mitchison, T.J.  
Cell 79, 449-458, 1994  
A:Title: A heterodimeric coiled-coil protein required for mitotic chromosome condensa  
A:Reference number: A55094; MUID:95042742  
A:Accession: B55094  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-1203 <HIR>  
A:Cross-references: GB:U13674; NID:9563813; PIDN:AAA64680.1; PID:9563814  
C:Superfamily: chromosome segregation protein SMCI  
C:Keywords: chromosomal protein; DNA condensation; heterodimer

Query Match 7.3%; Score 173.5; DB 2; Length 1203;  
Best Local Similarity 21.9%; Pred. No. 0.14;  
Matches 73; Conservative 69; Mismatches 135; Indels 57; Gaps 11;





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